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OM protein - protein search, using SW model

Run on: June 18, 2004, 12:57:29 ; Search time 23 Seconds
(without alignments)
17.957 Million cell updates/sec

Title: US-10-655-201-2

Perfect score: 44

Sequence: 1 KPSPPEE 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
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6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	9	4	US-09-101-2726-77
2	44	100.0	10	1	US-07-603-675-1
3	44	100.0	11	1	US-07-603-675-8
4	44	100.0	21	4	US-09-101-2726-38
5	44	100.0	157	3	US-08-142-5908-25
6	44	100.0	200	4	US-09-101-2726-73
7	44	100.0	208	4	US-09-101-2726-98
8	44	100.0	365	1	US-08-093-741-83
9	44	100.0	365	1	US-08-120-012-83
10	44	100.0	393	2	US-08-560-098A-44
11	44	100.0	393	3	US-08-967-024C-24
12	44	100.0	393	3	US-08-967-024C-25
13	44	100.0	411	1	US-08-087-163-1
14	44	100.0	411	1	US-08-286-748B-18
15	44	100.0	411	1	US-08-153-799-18
16	44	100.0	411	2	US-08-560-098A-48
17	44	100.0	411	3	US-09-181-816-1
18	44	100.0	411	4	US-09-403-736-2
19	44	100.0	430	1	US-07-942-157A-3
20	44	100.0	430	6	5219569-2
21	44	100.0	431	4	US-09-101-2726-1
22	44	100.0	431	6	5188829-1
23	44	100.0	432	3	US-08-560-098A-47
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26	36	81.8	362	4	US-09-875-114-1
27	36	81.8	418	2	US-08-257-963B-2

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29	36	81.8	418	4	US-08-520-373D-2	Sequence 2, Appl
30	36	81.8	418	5	PCT-US95-07201-2	Sequence 2, Appl
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34	35	79.5	19	3	US-08-394-748A-9	Sequence 9, Appl
35	35	79.5	19	4	US-09-675-922-13	Sequence 13, Appl
36	35	79.5	19	5	PCT-US93-11781-1	Sequence 1, Appl
37	35	79.5	19	5	PCT-US95-02478-9	Sequence 9, Appl
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39	35	79.5	271	3	US-08-536-891A-1	Sequence 1, Appl
40	35	79.5	271	3	US-08-533-100B-14	Sequence 14, Appl
41	35	79.5	271	4	US-09-366-009-1	Sequence 1, Appl
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45	35	79.5	368	2	US-08-836-854-17	Sequence 17, Appl
46	35	79.5	457	2	US-08-836-854-16	Sequence 16, Appl
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57	35	79.5	574	3	US-09-463-296-1	Sequence 1, Appl
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59	35	79.5	574	4	US-08-809-156B-24	Sequence 24, Appl
60	35	79.5	826	4	US-09-366-009-14	Sequence 14, Appl
61	35	79.5	826	4	US-08-809-156B-14	Sequence 14, Appl
62	35	79.5	896	4	US-09-585-858-17	Sequence 17, Appl
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64	35	79.5	1240	4	US-09-904-065-4	Sequence 4, Appl
65	35	79.5	1240	4	US-09-904-065-15	Sequence 15, Appl
66	35	79.5	1876	4	US-09-418-710-71	Sequence 71, Appl
67	35	79.5	1878	4	US-09-418-710-13	Sequence 13, Appl
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69	35	79.5	1911	2	US-08-800-825A-5	Sequence 5, Appl
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84	34	77.3	52	4	US-09-454-156A-5	Sequence 5, Appl
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94	34	77.3	336	2	US-08-474-379C-88	Sequence 88, Appl
95	34	77.3	382	4	US-09-533-029-92	Sequence 92, Appl
96	34	77.3	382	4	US-07-688-352C-40	Sequence 40, Appl
97	34	77.3	384	2	US-08-474-379C-40	Sequence 40, Appl
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103	34	77.3	500	1	US-08-375-510-1	Sequence 1, Appl1	176	32	72.7	1331	5	PCT-US95-07744A-3	Sequence 3, Appl1
104	34	77.3	500	2	US-08-487-657-1	Sequence 1, Appl1	177	32	72.7	1426	4	US-09-710-092-14	Sequence 14, Appl1
105	34	77.3	500	2	US-08-816-155B-45	Sequence 45, Appl1	178	32	72.7	2037	3	US-09-106-998-3	Sequence 3, Appl1
106	34	77.3	500	3	US-09-079-587-45	Sequence 45, Appl1	179	31	70.5	9	1	US-08-178-570-38	Sequence 38, Appl1
107	34	77.3	500	4	US-09-309-572-16	Sequence 16, Appl1	180	31	70.5	9	5	US-08-569-643-38	Sequence 38, Appl1
108	34	77.3	500	4	US-09-718-096-16	Sequence 16, Appl1	181	31	70.5	9	5	PCT-US95-00147-38	Sequence 38, Appl1
109	34	77.3	512	3	US-08-463-210-8	Sequence 8, Appl1	182	31	70.5	42	4	US-09-418-563-1	Sequence 1, Appl1
110	34	77.3	512	3	US-09-124-900-2	Sequence 2, Appl1	183	31	70.5	46	2	US-08-256-790-4	Sequence 4, Appl1
111	34	77.3	512	4	US-08-463-028-8	Sequence 8, Appl1	184	31	70.5	47	3	US-09-091-814-26	Sequence 26, Appl1
112	34	77.3	533	1	US-07-683-957B-3	Sequence 3, Appl1	185	31	70.5	47	4	US-09-205-258-507	Sequence 507, App
113	34	77.3	638	1	US-07-688-352C-22	Sequence 22, Appl1	186	31	70.5	47	4	US-09-205-258-513	Sequence 513, App
114	34	77.3	640	4	US-09-252-991A-19951	Sequence 19951, A	187	31	70.5	48	3	US-09-107-532A-35	Sequence 35, Appl1
115	34	77.3	686	2	US-08-942-521B-9	Sequence 9, Appl1	188	31	70.5	50	2	US-08-256-790-6	Sequence 6, Appl1
116	34	77.3	734	3	US-09-146-249A-85	Sequence 85, Appl1	189	31	70.5	53	2	US-08-256-790-8	Sequence 8, Appl1
117	34	77.3	734	3	US-08-206-188B-85	Sequence 85, Appl1	190	31	70.5	53	2	US-08-256-790-10	Sequence 10, Appl1
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119	34	77.3	885	2	US-09-079-630-33	Sequence 33, Appl1	192	31	70.5	85	4	US-09-252-991A-26629	Sequence 26629, A
120	34	77.3	886	2	US-08-474-379C-65	Sequence 65, Appl1	193	31	70.5	88	4	US-09-107-532A-3833	Sequence 3833, Ap
121	34	77.3	886	3	US-09-146-249A-65	Sequence 65, Appl1	194	31	70.5	95	4	US-09-252-991A-31932	Sequence 31932, A
122	34	77.3	886	3	US-08-206-188B-65	Sequence 65, Appl1	195	31	70.5	97	4	US-09-252-991A-23889	Sequence 23889, A
123	34	77.3	888	2	US-08-474-379C-12	Sequence 12, Appl1	196	31	70.5	99	4	US-09-107-532A-3698	Sequence 3698, Ap
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131	33	75.0	1301	4	US-09-071-035-238	Sequence 238, App	204	31	70.5	141	4	US-09-252-991A-15681	Sequence 15681, A
132	33	75.0	1301	4	US-09-071-035-242	Sequence 242, App	205	31	70.5	155	3	US-08-716-190-8	Sequence 8, Appl1
133	33	75.0	1306	4	US-09-134-000C-6670	Sequence 6670, Ap	206	31	70.5	157	3	US-08-683-2628-34	Sequence 34, Appl1
134	33	75.0	1306	4	US-09-134-000C-6588	Sequence 6588, Ap	207	31	70.5	161	2	US-08-683-2628-34	Sequence 34, Appl1
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136	32	72.7	138	4	US-09-148-545-222	Sequence 222, App	209	31	70.5	169	4	US-09-149-476-354	Sequence 354, App
137	32	72.7	139	4	US-09-148-545-160	Sequence 160, App	210	31	70.5	176	4	US-09-489-039A-11985	Sequence 11985, A
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139	32	72.7	243	1	US-07-869-933-29	Sequence 29, Appl1	212	31	70.5	202	4	US-09-252-991A-29946	Sequence 29946, A
140	32	72.7	243	1	US-07-869-933-33	Sequence 33, Appl1	213	31	70.5	222	4	US-09-227-357-161	Sequence 161, App
141	32	72.7	243	1	US-08-201-879A-4	Sequence 4, Appl1	214	31	70.5	255	3	US-09-040-485-2	Sequence 2, Appl1
142	32	72.7	243	2	US-08-916-902A-4	Sequence 4, Appl1	215	31	70.5	255	4	US-09-702-705-1806	Sequence 1806, Ap
143	32	72.7	243	2	US-09-213-389-4	Sequence 4, Appl1	216	31	70.5	255	4	US-09-736-457-1806	Sequence 1806, Ap
144	32	72.7	243	3	US-09-103-663-29	Sequence 29, Appl1	217	31	70.5	255	4	US-09-671-325-1806	Sequence 1806, Ap
145	32	72.7	243	3	US-09-103-663-33	Sequence 33, Appl1	218	31	70.5	261	4	US-09-205-258-505	Sequence 505, App
146	32	72.7	246	1	US-07-869-933-23	Sequence 23, Appl1	219	31	70.5	265	4	US-08-469-260A-77	Sequence 77, Appl1
147	32	72.7	246	3	US-09-103-663-23	Sequence 23, Appl1	220	31	70.5	265	4	US-08-488-446-77	Sequence 77, Appl1
148	32	72.7	306	2	US-08-560-098A-45	Sequence 45, Appl1	221	31	70.5	265	4	US-08-467-344A-77	Sequence 77, Appl1
149	32	72.7	331	2	US-08-560-098A-46	Sequence 46, Appl1	222	31	70.5	260	4	US-09-247-155-178	Sequence 178, App
150	32	72.7	427	4	US-09-506-066E-8	Sequence 8, Appl1	223	31	70.5	265	4	US-09-252-991A-19816	Sequence 19816, A
151	32	72.7	432	5	PCT-US95-04910-13	Sequence 13, Appl1	224	31	70.5	308	2	US-08-807-050-1	Sequence 1, Appl1
152	32	72.7	452	1	US-09-055-113-4	Sequence 4, Appl1	225	31	70.5	308	2	US-08-807-050-4	Sequence 4, Appl1
153	32	72.7	462	1	US-08-458-023B-2	Sequence 2, Appl1	226	31	70.5	308	2	US-08-807-050-4	Sequence 4, Appl1
154	32	72.7	463	3	US-09-111-556A-2	Sequence 2, Appl1	227	31	70.5	314	4	US-09-355-166-17	Sequence 17, Appl1
155	32	72.7	463	3	US-08-360-758-2	Sequence 2, Appl1	228	31	70.5	314	4	US-09-634-137-30	Sequence 30, Appl1
156	32	72.7	531	3	US-09-360-197-14	Sequence 14, Appl1	229	31	70.5	317	4	US-09-604-353-504	Sequence 504, App
157	32	72.7	571	4	US-09-252-991A-28549	Sequence 28549, A	230	31	70.5	319	4	US-09-252-991A-35635	Sequence 32635, A
158	32	72.7	622	4	US-09-338-352-4776	Sequence 4776, App	231	31	70.5	369	4	US-09-252-991A-20049	Sequence 20049, A
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160	32	72.7	685	2	US-08-878-989-1	Sequence 1, Appl1	233	31	70.5	370	4	US-09-252-991A-27810	Sequence 27810, A
161	32	72.7	685	3	US-09-136-282-2	Sequence 2, Appl1	234	31	70.5	373	4	US-09-066-281B-19	Sequence 19, Appl1
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163	32	72.7	685	3	US-09-505-744-2	Sequence 2, Appl1	236	31	70.5	375	4	US-09-552-991A-24278	Sequence 24278, A
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167	32	72.7	774	4	US-09-252-991A-16789	Sequence 16789, A	240	31	70.5	398	5	PCT-US91-0174E-20	Sequence 20, Appl1
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169	32	72.7	972	4	US-09-710-092-2	Sequence 2, Appl1	242	31	70.5	446	1	US-07-952-800-4	Sequence 4, Appl1
170	32	72.7	1056	4	US-09-710-092-6	Sequence 6, Appl1	243	31	70.5	448	4	US-08-216-592A-2	Sequence 2, Appl1
171	32	72.7	1130	4	US-09-976-594-860	Sequence 280, App	244	31	70.5	463	4	US-09-540-236-2942	Sequence 2942, Ap
172	32	72.7	1270	4	US-09-710-092-10	Sequence 10, Appl1	245	31	70.5	466	4	US-09-604-107A-8	Sequence 8, Appl1
173	32	72.7	1294	2	US-08-819-288-3	Sequence 3, Appl1	246	31	70.5	501	3	US-08-857-076-102	Sequence 102, App

247	31	70.5	510	5	PCT-US96-03916-3	Sequence 3, Appl1	320	30	68.2	217	4	US-08-467-602-399	Sequence 399, App
248	31	70.5	559	2	US-09-364-206-47	Sequence 47, Appl	321	30	68.2	217	4	US-08-467-602-413	Sequence 413, App
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250	31	70.5	560	3	US-08-808-323-18	Sequence 18, Appl	323	30	68.2	224	3	US-08-795-445A-50	Sequence 50, Appl
251	31	70.5	560	3	US-09-050-603A-18	Sequence 18, Appl	324	30	68.2	224	3	US-08-974-186-50	Sequence 50, Appl
252	31	70.5	560	3	US-09-102-420B-18	Sequence 18, Appl	325	30	68.2	224	3	US-08-974-186-50	Sequence 50, Appl
253	31	70.5	560	3	US-09-497-698-18	Sequence 18, Appl	326	30	68.2	224	3	US-08-795-445B-50	Sequence 50, Appl
254	31	70.5	575	4	US-09-171-461-30	Sequence 30, Appl	327	30	68.2	224	4	US-08-706-994A-137	Sequence 137, App
255	31	70.5	593	4	US-09-352-991A-23251	Sequence 23251, A	328	30	68.2	224	4	US-08-577-788B-51	Sequence 51, Appl
256	31	70.5	623	5	PCT-US96-03916-64	Sequence 64, Appl1	329	30	68.2	234	4	US-09-489-039A-12555	Sequence 12555, A
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ALIGNMENTS

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RESULT 1
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; Sequence 77, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nisissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
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; SEQ ID NO 77
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US-09-101-272G-77

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Query Match          100.0%; Score
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US-07-603-675-1
; Sequence 1, Application US/07603675
; Patent No. 5416006
; GENERAL INFORMATION:
; APPLICANT: Biasi, Francesco
; APPLICANT: Stoppelli, Maria P
; APPLICANT: Mastronicola, Maria R
; APPLICANT: Weindler, Karen G
; APPLICANT: Correas, Isabel
; TITLE OF INVENTION: MODIFICATION OF PLASMINOGEN ACTIVATORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/603,675
; FILING DATE: 19911218
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK90/00096
; FILING DATE: 11-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 644-0525
; TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: N
; FRAGMENT TYPE: Internal
; US-07-603-675-1
Query Match 100.0%; Score 44; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSSPPEE 8
DB 1 KPSSPPEE 8
RESULT 3
US-07-603-675-8
; Sequence 8, Application US/07603675
; Patent No. 5416006
; GENERAL INFORMATION:
; APPLICANT: Biasi, Francesco
; APPLICANT: Stoppelli, Maria P
; APPLICANT: Mastronicola, Maria R
; APPLICANT: Weindler, Karen G
; APPLICANT: Correas, Isabel
; TITLE OF INVENTION: MODIFICATION OF PLASMINOGEN ACTIVATORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK

STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/603,675
; FILING DATE: 19911218
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/DK90/00096
; FILING DATE: 11-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 644-0525
; TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: N
; FRAGMENT TYPE: Internal
; US-07-603-675-8
Query Match 100.0%; Score 44; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSSPPEE 8
DB 4 KPSSPPEE 11

RESULT 4
US-09-101-272G-38
; Sequence 38, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: 050979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; CURRENT FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 38
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Intervening sequence between formula 1 and formula 2
; US-09-101-272G-38
Query Match 100.0%; Score 44; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSSPPEE 8
DB 5 KPSSPPEE 12

RESULT 5
US-08-142-590B-25
; Sequence 25, Application US/08142590B
; Patent No. 6120765
; GENERAL INFORMATION:
; APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahiko; HORII, Izumi; and GOETINCK,
; TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,590B
; FILING DATE: 25-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,318
; FILING DATE: 02-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-009CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-142-590B-25

Query Match 100.0%; Score 44; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 136 KPSSPPE 143

RESULT 6
US-09-101-272G-73
; Sequence 73, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: 050979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; CURRENT FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 73
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: ATF domain of uPA
; US-09-101-272G-73

Query Match 100.0%; Score 44; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 156 KPSSPPE 163

RESULT 7
US-09-101-272G-98
; Sequence 98, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: 050979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; CURRENT FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 98
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ATFHI-ML chimeric protein
; US-09-101-272G-98

Query Match 100.0%; Score 44; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 137 KPSSPPE 144

RESULT 8
US-08-093-741-83
; Sequence 83, Application US/08093741
; Patent No. 5681721
; GENERAL INFORMATION:
; APPLICANT: STEFFENS, GERD J.
; APPLICANT: WENNDT, STEPHAN
; APPLICANT: SCHNEIDER, JOHANNES
; APPLICANT: HEINZEL-WIELAND, REGINA
; TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
; TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
; TITLE OF INVENTION: INHIBITING EFFECT
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N. W. Suite 700
; CITY: Washington, D.C.
; COUNTRY: U.S.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,741
; FILING DATE: 20-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P43 23 754.1
; FILING DATE: 15-JUL-1993

ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/41345
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-093-741-83

Query Match 100.0%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 90 KPSSPPEE 97

RESULT 9
US-08-720-012-83
Sequence 83, Application US/08720012
Patent No. 5747291
GENERAL INFORMATION:
APPLICANT: STEFFENS, GERT J.
APPLICANT: WENNDT, STEPHAN
APPLICANT: SCHNEIDER, JOHANNES
APPLICANT: HEINZEL-WIELAND, REGINA
APPLICANT: SAUNDERS, DEREK J.
TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N. W. Suite 700
CITY: Washington, D.C.
COUNTRY: U.S.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/720,012
FILING DATE: 27-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,741
FILING DATE: 20-JUL-1993
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/41345
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-720-012-83

Query Match 100.0%; Score 44; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 20;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KPSSPPEE 8
Db 90 KPSSPPEE 97

RESULT 10
US-08-560-098A-44
Sequence 44, Application US/08560098A
Patent No. 5976841
GENERAL INFORMATION:
APPLICANT: WENNDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gert Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-560-098A-44

Query Match 100.0%; Score 44; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 91 KPSSPPEE 98

RESULT 11
US-08-967-024C-24
Sequence 24, Application US/08967024C
Patent No. 6133011
GENERAL INFORMATION:
APPLICANT: WENNDT, Stephan
APPLICANT: STEFFENS, Gert Josef
APPLICANT: JANOCHA, Rike
APPLICANT: HEINZEL-WIELAND, Regina
TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:

ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 42 665.8
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42444
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-967-024C-24

Query Match 100.0%; Score 44; DB 3; Length 393;
Best local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
Db 91 KPSSPPEE 98

RESULT 12
US-08-967-024C-25
Sequence 25, Application US/08967024C
Patent No. 6133011
GENERAL INFORMATION:
APPLICANT: MNENDT, Stephan
APPLICANT: STEFFENS, Geird Josef
APPLICANT: JANCOCHA, Elke
APPLICANT: HEINZEL-WIELAND, Regina
TITLE OF INVENTION: Chimeric Proteins having fibrinolytic
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 42 665.8
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.

REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42444
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-967-024C-25

Query Match 100.0%; Score 44; DB 3; Length 393;
Best local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
Db 91 KPSSPPEE 98

RESULT 13
US-08-087-163-1
Sequence 1, Application US/08087163
Patent No. 5472692
GENERAL INFORMATION:
APPLICANT: Liu, Jian-Ning
APPLICANT: Gurewicz, Victor
TITLE OF INVENTION: PRO-UKROKINASE MUTANTS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,163
FILING DATE: 07/02/93
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Faese, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04353/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 411
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
US-08-087-163-1

Query Match 100.0%; Score 44; DB 1; Length 411;
Best local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
Db 91 KPSSPPEE 98

Db 136 KSPSPPEE 143

RESULT 14

US-08-286-748B-18
; Sequence 18, Application US/08286748B

; Patent No. 5759542

; GENERAL INFORMATION:

; APPLICANT: Victor Gurewlich

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY

; TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF

; TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 MB

; COMPUTER: IBM PS/2 Model 502 or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/286,748B

; FILING DATE: August 5, 1994

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: J. Peter Paease

; REGISTRATION NUMBER: 32,983

; REFERENCE/DOCKET NUMBER: 04547/013001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 411

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-286-748B-18

Query Match 100.0%; Score 44; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSPSPPEE 8

Db 136 KSPSPPEE 143

RESULT 15

US-08-153-799-18
; Sequence 18, Application US/08153799

; Patent No. 5766883

; GENERAL INFORMATION:

; APPLICANT: Ballance, David J

; APPLICANT: Goodey, Andrew R

; TITLE OF INVENTION: Polypeptides

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: R Hain Swope, BOC Health Care Inc

; STREET: 100 Mountain Avenue

; CITY: Murray Hill

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07974

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/153,799

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/847975

; FILING DATE: 06-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 8909916.2

; FILING DATE: 29-APR-1989

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB90/00650

; FILING DATE: 26-APR-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/775952

; FILING DATE: 29-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Swope, R Hain

; REGISTRATION NUMBER: 24864

; REFERENCE/DOCKET NUMBER: 92H832

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908) 665 2400

; TELEFAX: (908) 771 6159

; TELEX: 219484

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 411 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-153-799-18

Query Match 100.0%; Score 44; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSPSPPEE 8

Db 136 KSPSPPEE 143

RESULT 16

US-08-560-098A-48
; Sequence 48, Application US/08560098A

; Patent No. 5976841

; GENERAL INFORMATION:

; APPLICANT: WENDET, Stephan

; APPLICANT: HEINZEL-WIELAND, Regina

; APPLICANT: STEFFENS, Gerd Josef

; TITLE OF INVENTION: Proteins having fibrinolytic and

; TITLE OF INVENTION: Coagulation-inhibiting Properties

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan

; STREET: 1200 G Street, N.W., Suite 700

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/560,098A

; FILING DATE: 17-NOV-1995

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-560-098A-48

Query Match 100.0%; Score 44; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 136 KPSSPPE 143

RESULT 17
US-09-181-816-1
Sequence 1, Application US/09181816
Patent No. 6277818
GENERAL INFORMATION:
APPLICANT: MAZAR, Andrew P.
APPLICANT: JONES, Terence R.
TITLE OF INVENTION: CYCLIC PEPTIDE LIGANDS THAT TARGET UROKINASE
FILE REFERENCE: 32904200300 SIDN 1-7
CURRENT APPLICATION NUMBER: US/09/181,816
CURRENT FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 411
TYPE: PRT
ORGANISM: Homo sapiens
US-09-181-816-1

Query Match 100.0%; Score 44; DB 3; Length 411;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 136 KPSSPPE 143

RESULT 18
US-09-403-736-2
Sequence 2, Application US/09403736
Patent No. 6638502
GENERAL INFORMATION:
APPLICANT: Aventis S.A.
APPLICANT: Li, Hong
APPLICANT: GRISCELLI, Frank
APPLICANT: OPOLOU, Paule
APPLICANT: SORIA, Claudine
APPLICANT: RAGOT, Thierry
APPLICANT: LEGRAND, Yves
APPLICANT: SORIA, Jeanette
APPLICANT: MABILAT, Christelle
APPLICANT: PERRICAUDET, Michel
APPLICANT: YEH, Patrice

TITLE OF INVENTION: Adenovirus-Mediated Intratumoral Delivery Of An Angiogenesis Antag
TITLE OF INVENTION: For The Treatment Of Tumors
FILE REFERENCE: A2778A-US
CURRENT APPLICATION NUMBER: US/09/403,736
CURRENT FILING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: PCT/EP98/02491
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 60/044,980
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: humanurokinase
US-09-403-736-2

Query Match 100.0%; Score 44; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 136 KPSSPPE 143

RESULT 19
US-07-942-157A-3
Sequence 3, Application US/07942157A
Patent No. 5648253
GENERAL INFORMATION:
APPLICANT: Wei, Cha-Mer
TITLE OF INVENTION: Inhibitor-Resistant Urokinase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,157A
FILING DATE: 19920908
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/631673
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: TS1108cont.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)815-6508
TELEFAX: (404)815-6555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..19
OTHER INFORMATION: /label=peptide
OTHER INFORMATION: /note="MAP signal"
FEATURE:

NAME/KEY: Modified-site
LOCATION: 198..203
OTHER INFORMATION: /label= modified
OTHER INFORMATION: /note= "six amino acids deleted in mutant"
US-07-942-157A-3

Query Match 100.0%; Score 44; DB 1; Length 430;

Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 155 KPSSPPEE 162

RESULT 20
5219569-2
; Patent No. 5219569
; APPLICANT: BLABER, MICHAEL; HEYNEKER, HERBERT L.; VEHAR,
; GORDON A.
; TITLE OF INVENTION: PROTEASE RESISTANT UROKINASE
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/766,858
; FILING DATE: 16-AUG-1985
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 725,468
; FILING DATE: 22-APR-1985
; SEQ ID NO: 2
; LENGTH: 430
5219569-2

Query Match 100.0%; Score 44; DB 6; Length 430;

Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 155 KPSSPPEE 162

RESULT 21
US-09-101-272G-1
; Sequence 1, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; CURRENT FILING DATE: 1998-07-08
; PRIORITY APPLICATION NUMBER: JP 1059/1996
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 1
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (21)..()
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (20)..()
; OTHER INFORMATION: Urokinase-type plasminogen activator (uPA)
US-09-101-272G-1

Query Match 100.0%; Score 44; DB 4; Length 431;

Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8

Db 156 KPSSPPEE 163

RESULT 22
5188829-1
; Patent No. 5188829
; APPLICANT: KOBAYASHI, YO-ICHI; OMORI, MUNEKI; YAMADA, CHIKAKO
; TITLE OF INVENTION: RAPIDLY ACTING PROUROKINASE
; NUMBER OF SEQUENCES: 23
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/340,007
; FILING DATE: 18-AUG-1988
; SEQ ID NO: 1
; LENGTH: 431
5188829-1

Query Match 100.0%; Score 44; DB 6; Length 431;

Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 156 KPSSPPEE 163

RESULT 23
US-08-560-098A-47
; Sequence 47, Application US/08560098A
; Patent No. 5976841
; GENERAL INFORMATION:
; APPLICANT: MNENDT, Stephan
; APPLICANT: STEFFENS, Gerd Josef
; TITLE OF INVENTION: Proteins having Fibriolytic and
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,098A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 44 40 892.7
; FILING DATE: 17-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-560-098A-47

Query Match 100.0%; Score 44; DB 2; Length 432;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSSPPEE 8
|:|||||
Db 157 KPSSPPEE 164

RESULT 24
US-09-122-079-1
; Sequence 1, Application US/09122079
; Patent No. 6288024
; GENERAL INFORMATION:
; APPLICANT: Bouck, No. 62880241 P.
; APPLICANT: Dawson, David W.
; APPLICANT: Gillis, Paul R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING ANGIOGENESIS
; FILE REFERENCE: 87292
; CURRENT APPLICATION NUMBER: US/09/122,079
; PRIOR FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: US 08/899304
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-122-079-1

Query Match 81.8%; Score 36; DB 3; Length 362;
Best Local Similarity 85.7%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSSPPEE 8
|:|||||
Db 22 PSSPPEE 28

RESULT 25
US-09-875-223-1
; Sequence 1, Application US/09875223
; Patent No. 6391850
; GENERAL INFORMATION:
; APPLICANT: No. 6391850thwestern University
; APPLICANT: No. 63918501 Bouck
; APPLICANT: David Dawson
; APPLICANT: Paul Gillis
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Angiogenesis
; FILE REFERENCE: 0290-2303
; CURRENT APPLICATION NUMBER: US/09/875,223
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 09/122,079
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: PCT/US98/15228
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: US 08/899,304
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-223-1

Query Match 81.8%; Score 36; DB 4; Length 362;
Best Local Similarity 85.7%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSSPPEE 8
|:|||||
Db 22 PSSPPEE 28

RESULT 26
US-09-875-114-1
; Sequence 1, Application US/09875114
; Patent No. 6670333
; GENERAL INFORMATION:
; APPLICANT: No. 6670333thwestern University
; APPLICANT: No. 66703331 Bouck
; APPLICANT: David Dawson
; APPLICANT: Paul Gillis
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Angiogenesis
; FILE REFERENCE: 0290-2302
; CURRENT APPLICATION NUMBER: US/09/875,114
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 09/122,079
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: PCT/US98/15228
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: US 08/899,304
; PRIOR FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 362
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-114-1

Query Match 81.8%; Score 36; DB 4; Length 362;
Best Local Similarity 85.7%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSSPPEE 8
|:|||||
Db 22 PSSPPEE 28

RESULT 27
US-08-257-963B-2
; Sequence 2, Application US/08257963B
; Patent No. 5840686
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Becerra, S.
; APPLICANT: Patricia; Schwartz, Joan P.;
; APPLICANT: Taniwaki, Takayuki
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
; TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
; TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Avenue
; City: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; OPERATING SYSTEM: IBM PC Compatible
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,963B
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEPT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36434
; REFERENCE/DOCKET NUMBER: 20264126US1

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: CDS
LOCATION: 117..1373
OTHER INFORMATION: /note="product =
OTHER INFORMATION: "pigment epithelial-derived factor"
OTHER INFORMATION: gene = "PEDF" codon_start = 1"
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 117..170
OTHER INFORMATION: PEDF amino acid
OTHER INFORMATION: sequence
US-08-257-963B-2

Query Match
Best Local Similarity 81.8%; Score 36; DB 2; Length 418;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSSPPEE 8
Db 22 PASPPEE 28

RESULT 28
US-08-367-841A-2
Sequence 2, Application US/08367841A
Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez,
APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Tombran-Tink, Joyce
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA: 07/952,796
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 751-6849
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
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SEQUENCE CHARACTERISTICS:
LENGTH: 418 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: CDS
LOCATION: 117..1373
OTHER INFORMATION: /note="product =
OTHER INFORMATION: "pigment epithelial-derived factor"
OTHER INFORMATION: gene = "PEDF" codon_start = 1"
FEATURE:
NAME/KEY:
LOCATION:
OTHER INFORMATION: PEDF amino acid
OTHER INFORMATION: sequence
US-08-367-841A-2

Query Match
Best Local Similarity 81.8%; Score 36; DB 4; Length 418;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSSPPEE 8
Db 22 PASPPEE 28

RESULT 29
US-08-520-373D-2
Sequence 2, Application US/08520373D
Patent No. 6451763
GENERAL INFORMATION:
APPLICANT: Tombran-Tink, Joyce
APPLICANT: Steele, Finlan R
APPLICANT: Chader, Gerald J
APPLICANT: Becerra, Sofia P
APPLICANT: Johnson, Lincoln V
APPLICANT: Rodriguez, Ignacio R
TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
FILE REFERENCE: 2026-4203US1
CURRENT APPLICATION NUMBER: US/08/520,373D
CURRENT FILING DATE: 1995-08-29
PRIOR APPLICATION NUMBER: 08/377,710
PRIOR FILING DATE: 1995-01-25
PRIOR APPLICATION NUMBER: 08/279,979
PRIOR FILING DATE: 1994-07-25
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR FILING DATE: 1992-06-04
PRIOR APPLICATION NUMBER: 07/952,796
PRIOR FILING DATE: 1992-09-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 418
TYPE: PRT
ORGANISM: HUMAN
US-08-520-373D-2

Query Match
Best Local Similarity 81.8%; Score 36; DB 4; Length 418;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSSPPEE 8
Db 22 PASPPEE 28

RESULT 30
PCT-US95-07201-2
Sequence 2, Application PC/TUS9507201
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Patricia, Schwartz, Joan P.;
```

```

;
; APPLICANT: Taniwaki, Takayuki
; TITLE OF INVENTION: PIGMENT EPITHELIAL
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07201
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/367,841
; FILING DATE: 30-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,963
; FILING DATE: 07-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36434
; REFERENCE/DOCKET NUMBER: 20264126PCT
; TELEPHONE: (212) 751-6849
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 418 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 117..1373
; OTHER INFORMATION: /note= "product =
; OTHER INFORMATION: "pigment epithelial-derived factor"
; OTHER INFORMATION: gene = "PEDF" codon_start = 1"
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: PEDF amino acid
; OTHER INFORMATION: sequence
; PCT-US95-07201-2
;
; Query Match 81.8%; Score 36; DB 5; Length 418;
; Best Local Similarity 85.7%; Pred. No. 3.5e+02;
; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
;
; QY 2 PSSPPE 8
; Db 22 PSSPPE 28
;
; RESULT 31
; US-08-291-349A-1
; Sequence 1, Application US/08291349A
; Patent No. 5545620
; GENERAL INFORMATION:
; APPLICANT: Wahl, Sharon M.
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; COUNTRY: USA

```

```

;
; TITLE OF INVENTION: Synthetic Fibronectin Fragments As
; TITLE OF INVENTION: Inhibitors of Retroviral Infection
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allgretti & Witcoff
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,349A
; FILING DATE: 16 AUG 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/006,121
; FILING DATE: 19 JAN 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDowell, John J.
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,673-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..19
; OTHER INFORMATION: /note= "FNI (1906-1924)
; OTHER INFORMATION: fibronectin fragment : FN-C/H-I"
; US-08-291-349A-1
;
; Query Match 79.5%; Score 35; DB 1; Length 19;
; Best Local Similarity 75.0%; Pred. No. 24;
; Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
;
; QY 1 KPSSPPE 8
; Db 3 KPSSPPE 10
;
; RESULT 32
; US-07-990-296-1
; Sequence 1, Application US/07990296
; Patent No. 5591719
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: Allen, Janice B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: McCarthy, James B.
; TITLE OF INVENTION: Method for Treating Acute and
; TITLE OF INVENTION: Chronic Inflammatory Disorders using Polypeptides
; TITLE OF INVENTION: with Fibronectin Activity
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5591719west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA

```

ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/990,296
FILING DATE: 19921210
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Alan W.
REGISTRATION NUMBER: 31,535
REFERENCE/DOCKET NUMBER: 600,252-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acid residues
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: Peptide
FRAGMENT TYPE: Internal Fragment
ORIGINAL SOURCE: Synthetically Derived
FEATURE:
NAME/KEY: Fragment of the 33 kD carboxy
terminal heparin-binding fragment of the A
NAME/KEY: chain of fibronectin
LOCATION: Represents isolated fibronectin
LOCATION: residues 1906-1924 from all plasma isoforms
LOCATION: of fibronectin
US-07-990-296-1

Query Match 79.5%; Score 35; DB 1; Length 19;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSSPPE 8
Db 3 KPSSPPE 10

RESULT 33
US-08-480-133A-1
Sequence 1, Application US/08460133A
Patent No. 5840691
GENERAL INFORMATION:
APPLICANT: Furcht, Leo T.
APPLICANT: McCarthy, James B.
APPLICANT: Wahl, Sharon M.
APPLICANT: Allen, Janice B.
APPLICANT: Billups, Kevin L.
APPLICANT: Everett, Jeffrey E.
TITLE OF INVENTION: Method for Treating Inflammatory
TITLE OF INVENTION: Diseases Using Polypeptides with Fibronectin Activity
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5840691west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,133A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,903
FILING DATE: 21-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,296
FILING DATE: 10-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 600-308US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-480-133A-1

Query Match 79.5%; Score 35; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSSPPE 8
Db 3 KPSSPPE 10

RESULT 34
US-08-394-748A-9
Sequence 9, Application US/08394748A
Patent No. 6013628
GENERAL INFORMATION:
APPLICANT: Skubitz, Amy P.N.
APPLICANT: Furcht, Leo T.
APPLICANT: Balles, Mark
APPLICANT: Gregerson, Dale S.
APPLICANT: Agarwal, Anita
APPLICANT: Wright, Martha M.
APPLICANT: Murali, Shobana
TITLE OF INVENTION: Method for Treating Conditions of the Eye
TITLE OF INVENTION: Using Polypeptides
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 6013628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,748A
FILING DATE: 27-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/203,458
FILING DATE: 28-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 600.307US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE: FN-C/H-1
US-08-394-748A-9

Query Match 79.5%; Score 35; DB 3; Length 19;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 3 KPSSPPE 10

RESULT 35
US-09-675-922-13
Sequence 13, Application US/09675922
Patent No. 6468731
GENERAL INFORMATION:
APPLICANT: Hubbell A., Jeffrey
APPLICANT: Schense C., Jason
APPLICANT: Sakiyama E., Shelley
TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for Tissue
TITLE OF INVENTION: Engineering: Incorporation of Proteins
FILE REFERENCE: ETH 107 DIV
CURRENT APPLICATION NUMBER: US/09/675,922
CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: heparin-binding sequence
US-09-675-922-13

Query Match 79.5%; Score 35; DB 4; Length 19;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 3 KPSSPPE 10

RESULT 36
PCT-US93-11781-1
Sequence 1, Application PC/TUS9311781
GENERAL INFORMATION:
APPLICANT: Regents of the University of Minnesota
APPLICANT: Morrill Hall
APPLICANT: 100 Church Street, S.E.
APPLICANT: Minneapolis, Minnesota 55455
APPLICANT: U.S.A.
APPLICANT: Represented By The Secretary of Health
APPLICANT: and Human Services
APPLICANT: 200 Independence Avenue S.W.
APPLICANT: Washington, D.C. 20201
APPLICANT: United States of America
TITLE OF INVENTION: Polypeptides Useful for Treating
TITLE OF INVENTION: Inflammatory Disorders
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 Norwest Center
CITY: Minneapolis
STATE: MN

COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11781
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,903
FILING DATE: 21-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,296
FILING DATE: 10-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kowalczyk, Alan W.
REGISTRATION NUMBER: 31,535
REFERENCE/DOCKET NUMBER: 600,283-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11781-1

Query Match 79.5%; Score 35; DB 5; Length 19;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 3 KPSSPPE 10

RESULT 37
PCT-US95-02478-9
Sequence 9, Application PC/TUS9502478
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method for Treating Conditions
TITLE OF INVENTION: Of the Eye Using Polypeptides
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/203,458
FILING DATE: 28-FEB-1994
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
STRAIN: FN-C/H-1
PCT-US95-02478-9

Query Match 79.5%; Score 35; DB 5; Length 19;
Best Local Similarity 75.0%; Pred. No. 24;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSPPE 8
|||
Db 3 KPSPPE 10

RESULT 38

US-09-252-991A-29265

Sequence 29265, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfeld et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29265

LENGTH: 150

TYPE: PR

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-29265

Query Match 79.5%; Score 35; DB 4; Length 150;

Best Local Similarity 75.0%; Pred. No. 1.8e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSPPE 8

|||

Db 104 KPSPPE 111

RESULT 39

US-08-536-891A-1

Sequence 1, Application US/08536891A

Patent No. 6033907

GENERAL INFORMATION:

APPLICANT: David A. Williams

TITLE OF INVENTION: Enhanced Virus-Mediated DNA Transfer

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Thomas Q. Henry

STREET: Bank One Tower, Suite 3700, 111 Monument Circle

CITY: Indianapolis

STATE: Indiana

COUNTRY: USA

ZIP: 46204

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage

COMPUTER: COMPAQ

OPERATING SYSTEM: MSDOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/536,891A

FILING DATE: September 29, 1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/03817

FILING DATE: March 27, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/218,355

FILING DATE: March 25, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Thomas Q. Henry

REGISTRATION NUMBER: 28,309

REFERENCE/DOCKET NUMBER: 7037-52/IU-33-CIP-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 634-3456
TELEFAX: (317) 637-7561
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein fragment

US-08-536-891A-1

Query Match 79.5%; Score 35; DB 3; Length 271;

Best Local Similarity 75.0%; Pred. No. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSPPE 8

|||

Db 219 KPSPPE 226

RESULT 40

US-08-933-100B-14

Sequence 14, Application US/08933100B

Patent No. 6274704

GENERAL INFORMATION:

APPLICANT: FUKAI, FUMIO

APPLICANT: KATAYAMA, TAKASHI

TITLE OF INVENTION: BIOLOGICALLY ACTIVE PEPTIDE AND CANCER

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: PILLSBURY, MADISON & SUTRO

STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/933,100B

FILING DATE: 18-SEP-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: PERRY, GLENN

REGISTRATION NUMBER: 28458

REFERENCE/DOCKET NUMBER: 7898/242094

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000

TELEFAX: 202-822-0944

TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 271

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

FEATURE: OTHER INFORMATION: sequence of a part (1600-1870) of Heparin binding site

US-08-933-100B-14

Query Match 79.5%; Score 35; DB 3; Length 271;

Best Local Similarity 75.0%; Pred. No. 3.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSPPE 8

|||

Db 219 KPSPPE 226

RESULT 41
US-09-366-009-1
; Sequence 1, Application US/09366009
; Patent No. 6426042
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Koyama, No. 6426042uto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/366, 009
; FILING DATE: 02-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: peptide
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-366-009-1
Query Match 79.5%; Score 35; DB 4; Length 271;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
DB 219 KPSSPPE 226

RESULT 42
US-08-809-156B-1
; Sequence 1, Application US/08809156B
; Patent No. 6472204
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Koyama, No. 6472204uto
; Hashino, Kimikazu
; APPLICANT: Ueno, Takashi
; Koyama, No. 6472204uto
; APPLICANT: Hashino, Kimikazu

APPLICANT: Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,156B
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/03254
; FILING DATE: 07-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE: peptide
; TOPOLOGY: linear
; US-08-809-156B-1
Query Match 79.5%; Score 35; DB 4; Length 271;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
DB 219 KPSSPPE 226

RESULT 43
US-09-043-981-1
; Sequence 1, Application US/09043981
; Patent No. 6670177
; GENERAL INFORMATION:
; APPLICANT: Williams, David A.
; TITLE OF INVENTION: METHODS FOR ENHANCED VIRUS MEDIATED DNA TRANSFER USING
; FILE REFERENCE: 7037-297
; CURRENT APPLICATION NUMBER: US/09/043,981
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US96/15712
; EARLIER FILING DATE: 1996-09-30
; EARLIER APPLICATION NUMBER: 08/536,891
; EARLIER FILING DATE: 1995-09-29
; EARLIER APPLICATION NUMBER: 60/024,169
; EARLIER FILING DATE: 1996-08-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1
LENGTH: 271
TYPE: PRT
ORGANISM: Homo sapiens
US-09-043-981-1

Query Match 79.5%; Score 35; DB 4; Length 271;
Best Local Similarity 75.0%; Pred. No. 3.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
DB 219 KPSPPEE 226

RESULT 44
US-08-836-854-4
Sequence 4, Application US/08836854
Patent No. 5824547
GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION DATA: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: HASHINO=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 296 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-854-4

Query Match 79.5%; Score 35; DB 2; Length 296;
Best Local Similarity 75.0%; Pred. No. 3.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
DB 219 KPSPPEE 226

RESULT 45

US-08-836-854-17
Sequence 17, Application US/08836854
Patent No. 5824547
GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION DATA: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: HASHINO=1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-854-17

Query Match 79.5%; Score 35; DB 2; Length 368;
Best Local Similarity 75.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
DB 316 KPSPPEE 323

RESULT 46
US-08-836-854-16
Sequence 16, Application US/08836854
Patent No. 5824547
GENERAL INFORMATION:
APPLICANT: HASHINO, Kimikazu
APPLICANT: MATSUSHITA, Hideyuki
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street N.W. Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,854
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/02425
FILING DATE: 29-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 317721/1994
FILING DATE: 29-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: HASHINO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-854-16

Query Match 79.5%; Score 35; DB 2; Length 457;
Best Local Similarity 75.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
DB 405 KPSSPPE 412

RESULT 47
US-09-366-009-22
Sequence 22, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Koyama, No. 6426042uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-AUG-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>

APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-366-009-22

Query Match 79.5%; Score 35; DB 4; Length 457;
Best Local Similarity 75.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
DB 405 KPSSPPE 412

RESULT 48
US-08-809-156B-22
Sequence 22, Application US/08809156B
Patent No. 6472204
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
APPLICANT: Uemori, Takashi
APPLICANT: Koyama, No. 6472204uto
APPLICANT: Hashino, Kimikazu
APPLICANT: Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,156B
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03254
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-809-156B-22

Query Match 79.5%; Score 35; DB 4; Length 457;
Best Local Similarity 75.0%; Pred. No. 5.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
DB 405 KPSPPRE 412

RESULT 49
US-09-366-009-13
Sequence 13, Application US/09366009
Patent No. 6426042
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Koyama, No. 6426042uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/366,009
FILING DATE: 02-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,156
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 547 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-366-009-13

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Best Local Similarity 75.0%; Pred. No. 6.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
DB 222 KPSPPRE 229

RESULT 50
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Sequence 13, Application US/08809156B
Patent No. 6472204
GENERAL INFORMATION:
APPLICANT: Asada, Kiyozo
Uemori, Takashi
Koyama, No. 6472204uto
Hashino, Kimikazu
Kato, Ikunoshin
TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,156B
FILING DATE: 07-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/03254
FILING DATE: 07-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 294382/1995
FILING DATE: 13-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 051847/1996
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 977.6507P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 547 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-809-156B-13

Query Match 79.5%; Score 35; DB 4; Length 547;
Best Local Similarity 75.0%; Pred. No. 6.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
DB 222 KPSPPRE 229

Search completed: June 18, 2004, 13:00:59
Job time : 27 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 12:58:49 ; Search time 43 Seconds
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Title: US-10-655-201-2
Perfect score: 44
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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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141	36	81.8	1089	14	US-10-176-482-266	Sequence 266, App	214	36	81.8	1089	14	US-10-183-013-266	Sequence 266, App
142	36	81.8	1089	14	US-10-176-757-266	Sequence 266, App	215	36	81.8	1089	14	US-10-184-612-266	Sequence 266, App
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145	36	81.8	1089	14	US-10-180-557-266	Sequence 266, App	218	36	81.8	1089	14	US-10-184-622-266	Sequence 266, App
146	36	81.8	1089	14	US-10-173-700-266	Sequence 266, App	219	36	81.8	1089	14	US-10-184-628-266	Sequence 266, App
147	36	81.8	1089	14	US-10-174-572-266	Sequence 266, App	220	36	81.8	1089	14	US-10-184-630-266	Sequence 266, App
148	36	81.8	1089	14	US-10-174-579-266	Sequence 266, App	221	36	81.8	1089	14	US-10-184-632-266	Sequence 266, App
149	36	81.8	1089	14	US-10-174-582-266	Sequence 266, App	222	36	81.8	1089	14	US-10-184-631-266	Sequence 266, App
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152	36	81.8	1089	14	US-10-175-740-266	Sequence 266, App	225	36	81.8	1089	14	US-10-184-640-266	Sequence 266, App
153	36	81.8	1089	14	US-10-175-743-266	Sequence 266, App	226	36	81.8	1089	14	US-10-184-650-266	Sequence 266, App
154	36	81.8	1089	14	US-10-176-488-266	Sequence 266, App	227	36	81.8	1089	14	US-10-184-651-266	Sequence 266, App
155	36	81.8	1089	14	US-10-176-492-266	Sequence 266, App	228	36	81.8	1089	14	US-10-187-588-266	Sequence 266, App
156	36	81.8	1089	14	US-10-176-747-266	Sequence 266, App	229	36	81.8	1089	14	US-10-187-597-266	Sequence 266, App
157	36	81.8	1089	14	US-10-176-750-266	Sequence 266, App	230	36	81.8	1089	14	US-10-187-598-266	Sequence 266, App
158	36	81.8	1089	14	US-10-176-985-266	Sequence 266, App	231	36	81.8	1089	14	US-10-187-600-266	Sequence 266, App
159	36	81.8	1089	14	US-10-176-987-266	Sequence 266, App	232	36	81.8	1089	14	US-10-187-601-266	Sequence 266, App
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161	36	81.8	1089	14	US-10-176-993-266	Sequence 266, App	234	36	81.8	1089	14	US-10-187-603-266	Sequence 266, App

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236	36	81.8	1089	14	US-10-187-743-266	Sequence 266, App	309	36	81.8	1089	14	US-10-194-485-266	Sequence 266, App
237	36	81.8	1089	14	US-10-187-746-266	Sequence 266, App	310	36	81.8	1089	14	US-10-195-883-266	Sequence 266, App
238	36	81.8	1089	14	US-10-187-747-266	Sequence 266, App	311	36	81.8	1089	14	US-10-195-899-266	Sequence 266, App
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240	36	81.8	1089	14	US-10-187-753-266	Sequence 266, App	313	36	81.8	1089	14	US-10-196-750-266	Sequence 266, App
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242	36	81.8	1089	14	US-10-187-757-266	Sequence 266, App	315	36	81.8	1089	14	US-10-197-700-266	Sequence 266, App
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253	36	81.8	1089	14	US-10-195-902-266	Sequence 266, App	326	36	81.8	1089	14	US-10-199-314-266	Sequence 266, App
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257	36	81.8	1089	14	US-10-176-479-266	Sequence 266, App	330	36	81.8	1089	14	US-10-199-669-266	Sequence 266, App
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262	36	81.8	1089	14	US-10-179-519-266	Sequence 266, App	335	36	81.8	1089	14	US-10-202-469-266	Sequence 266, App
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264	36	81.8	1089	14	US-10-180-540-266	Sequence 266, App	337	36	81.8	1089	14	US-10-202-476-266	Sequence 266, App
265	36	81.8	1089	14	US-10-180-545-266	Sequence 266, App	338	36	81.8	1089	14	US-10-202-934-266	Sequence 266, App
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268	36	81.8	1089	14	US-10-183-017-266	Sequence 266, App	341	36	81.8	1089	14	US-10-202-939-266	Sequence 266, App
269	36	81.8	1089	14	US-10-183-019-266	Sequence 266, App	342	36	81.8	1089	14	US-10-205-509-266	Sequence 266, App
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274	36	81.8	1089	14	US-10-184-627-266	Sequence 266, App	347	36	81.8	1089	14	US-10-184-638-266	Sequence 266, App
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277	36	81.8	1089	14	US-10-184-655-266	Sequence 266, App	350	36	81.8	1089	14	US-10-184-602-266	Sequence 266, App
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281	36	81.8	1089	14	US-10-196-745-266	Sequence 266, App	354	36	81.8	1089	14	US-10-187-752-266	Sequence 266, App
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292	36	81.8	1089	14	US-10-179-522-266	Sequence 266, App	365	36	81.8	1089	14	US-10-201-324-266	Sequence 266, App
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295	36	81.8	1089	14	US-10-183-015-266	Sequence 266, App	368	36	81.8	1089	14	US-10-201-528-266	Sequence 266, App
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297	36	81.8	1089	14	US-10-184-620-266	Sequence 266, App	370	36	81.8	1089	14	US-10-201-530-266	Sequence 266, App
298	36	81.8	1089	14	US-10-184-643-266	Sequence 266, App	371	36	81.8	1089	14	US-10-202-408-266	Sequence 266, App
299	36	81.8	1089	14	US-10-184-656-266	Sequence 266, App	372	36	81.8	1089	14	US-10-202-409-266	Sequence 266, App
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301	36	81.8	1089	14	US-10-205-908-266	Sequence 266, App	374	36	81.8	1089	14	US-10-202-472-266	Sequence 266, App
302	36	81.8	1089	14	US-10-184-619-266	Sequence 266, App	375	36	81.8	1089	14	US-10-205-502-266	Sequence 266, App
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304	36	81.8	1089	14	US-10-187-599-266	Sequence 266, App	377	36	81.8	1089	14	US-10-205-511-266	Sequence 266, App
305	36	81.8	1089	14	US-10-187-780-266	Sequence 266, App	378	36	81.8	1089	14	US-10-205-902-266	Sequence 266, App
306	36	81.8	1089	14	US-10-192-015-266	Sequence 266, App	379	36	81.8	1089	14	US-10-205-907-266	Sequence 266, App
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OTHER INFORMATION: positions 136-143 of uPA
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)_RES
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)_RES
OTHER INFORMATION: AMIDATION
US-10-235-552-2

Query Match 100.0%; Score 44; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
Db 1 KPSSPPEE 8

RESULT 2
US-10-235-552-1
Sequence 1, Application US/10235552
Publication No. US20030027768A1
GENERAL INFORMATION:
APPLICANT: Mazar, Andrew P.
TITLE OF INVENTION: ANTI-INVASIVE AND ANTI-ANGIOGENIC COMPOSITIONS AND METHODS
FILE REFERENCE: 38369-183655
CURRENT APPLICATION NUMBER: US/10/235,552
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 08/900,327
PRIOR FILING DATE: 1997-07-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: corresponds to
OTHER INFORMATION: positions 136-145 of the human protein urokinase
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (10)
OTHER INFORMATION: AMIDATION
US-10-235-552-1

Query Match 100.0%; Score 44; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
Db 1 KPSSPPEE 8

RESULT 3
US-09-880-503-9
Sequence 9, Application US/09880503
Patent No. US20020131964A1
GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503

CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 96
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-503-9

Query Match 100.0%; Score 44; DB 9; Length 96;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
Db 89 KPSSPPEE 96

RESULT 4
US-09-880-503-8
Sequence 8, Application US/09880503
Patent No. US20020131964A1
GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-503-8

Query Match 100.0%; Score 44; DB 9; Length 143;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
Db 136 KPSSPPEE 143

RESULT 5
US-09-880-503-5
Sequence 5, Application US/09880503
Patent No. US20020131964A1
GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-503-5

Query Match 100.0%; Score 44; DB 9; Length 276;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 1 KPSSPPE 8

RESULT 6
US-09-880-503-7

; Sequence 7, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880,503
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/212,847
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-7

Query Match 100.0%; Score 44; DB 9; Length 323;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 48 KPSSPPE 55

RESULT 7
US-10-106-698-6266

; Sequence 6266, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005PI
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patentin Ver. 3.0
; SEQ ID NO 6266
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-6266

Query Match 100.0%; Score 44; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 162 KPSSPPE 169

RESULT 8
US-10-264-049-2927

; Sequence 2927, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PI
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 2927
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2927

Query Match 100.0%; Score 44; DB 15; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 162 KPSSPPE 169

RESULT 9
US-09-880-503-3

; Sequence 3, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880,503
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/212,847
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-3

Query Match 100.0%; Score 44; DB 9; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 136 KPSSPPE 143

RESULT 10
US-10-407-821-2

; Sequence 2, Application US/10407821
; Publication No. US20030219386A1
; GENERAL INFORMATION:
; APPLICANT: IDELL, STEVEN
; TITLE OF INVENTION: INTRAPLEURAL SINGLE-CHAIN UROKINASE ALONE OR COMPLEXED
; TITLE OF INVENTION: TO ITS SOLUBLE RECEPTOR PROTECTS AGAINST PLEURAL
; FILE REFERENCE: UTSN:022US
; CURRENT APPLICATION NUMBER: US/10/407,821

```

; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/414,202
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/370,466
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-407-821-2

```

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Query Match
Best Local Similarity 100.0%; Score 44; DB 15; Length 411;
Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

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QY 1 KPSSPEE 8
Db 136 KPSSPEE 143

```

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RESULT 11
US-10-372-966-6
; Sequence 6, Application US/10372966
; Publication No. US20040111765A1
; GENERAL INFORMATION:
; APPLICANT: OISHI, Karen K.
; APPLICANT: ZHOU, Da-Feng
; TITLE OF INVENTION: PRODUCTION OF UROKINASE IN PLANT-BASED EXPRESSION
; FILE REFERENCE: 048281/0107
; CURRENT APPLICATION NUMBER: US/10/372,966
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US/09/344,376
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/091,911
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Human
; US-10-372-966-6

```

```

Query Match
Best Local Similarity 100.0%; Score 44; DB 16; Length 411;
Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

```

```

QY 1 KPSSPEE 8
Db 137 KPSSPEE 144

```

```

RESULT 12
US-10-372-966-4
; Sequence 4, Application US/10372966
; Publication No. US20040111765A1
; GENERAL INFORMATION:
; APPLICANT: OISHI, Karen K.
; APPLICANT: ZHOU, Da-Feng
; TITLE OF INVENTION: PRODUCTION OF UROKINASE IN PLANT-BASED EXPRESSION
; FILE REFERENCE: 048281/0107
; CURRENT APPLICATION NUMBER: US/10/372,966
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US/09/344,376
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/091,911
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0

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; SEQ ID NO 4
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Human
; US-10-372-966-4

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```

Query Match
Best Local Similarity 100.0%; Score 44; DB 16; Length 430;
Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

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QY 1 KPSSPEE 8
Db 156 KPSSPEE 163

```

```

RESULT 13
US-09-264-468B-1
; Sequence 1, Application US/09264468B
; Patent No. US20020106775A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Jieyi
; APPLICANT: Niemeyer, Vicki L.
; APPLICANT: Henkin, Jack
; APPLICANT: Smith, Richard A.
; APPLICANT: Walter, Karl A.
; APPLICANT: Severin, Jean M.
; APPLICANT: Edalji, Rohinton
; APPLICANT: Johnson Jr., Robert W.
; APPLICANT: Holzman, Thomas F.
; TITLE OF INVENTION: HIGHLY CRYSTALLINE UROKINASE
; FILE REFERENCE: 6310.US.P1
; CURRENT APPLICATION NUMBER: US/09/264,468B
; CURRENT FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 09/036,361
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1) ... (20)
; OTHER INFORMATION: Leader sequence
; NAME/KEY: VARIANT
; LOCATION: (279) ... (279)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: VARIANT
; LOCATION: (302) ... (302)
; OTHER INFORMATION: Xaa = any amino acid
; US-09-264-468B-1

```

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Query Match
Best Local Similarity 100.0%; Score 44; DB 9; Length 431;
Pred. No. 1.3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

```

```

QY 1 KPSSPEE 8
Db 156 KPSSPEE 163

```

```

RESULT 14
US-10-411-037-34
; Sequence 34, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi

```

APPLICANT: Bove, Caryn
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
FILE REFERENCE: 040853-01-5082
CURRENT APPLICATION NUMBER: US/10/411,037
PRIOR FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/348,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
US-10-411-037-34

Query Match 100.0%; Score 44; DB 12; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
DB 156 KPSSPPE 163

RESULT 15
US-10-411-026-34
Sequence 34, Application US/10411026
Publication No. US2004006391A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
FILE REFERENCE: 040853-01-5053
CURRENT APPLICATION NUMBER: US/10/411,026
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens

US-10-411-026-34
Query Match 100.0%; Score 44; DB 12; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
DB 156 KPSSPPE 163

RESULT 16
US-10-282-174-562
Sequence 562, Application US/10282174
Publication No. US20030224380A1
GENERAL INFORMATION:
APPLICANT: Becker, Kenneth David
APPLICANT: Veliceladi, Gonul
APPLICANT: Elliot, Kathryn J.
APPLICANT: Wang, Xin
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Bertram, Lars
APPLICANT: Saunders, Aleister J.
APPLICANT: Mullin, Kristina M.
APPLICANT: Sampson, Andrew Johnson
APPLICANT: Blacker, Deborah Lynne
TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
FILE REFERENCE: 37481-3308
CURRENT APPLICATION NUMBER: US/10/282,174
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: US 60/339,525
PRIOR FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: US 60/338,010
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/336,929
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/338,363
PRIOR FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: US 60/337,052
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: US 60/368,919
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 564
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 562
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: 15, 58, 141, 214, 231, 274, 366
OTHER INFORMATION: xaa = Any Amino Acid
US-10-282-174-562

Query Match 100.0%; Score 44; DB 12; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
DB 156 KPSSPPE 163

RESULT 17
US-10-076-421-2
Sequence 2, Application US/10076421
Publication No. US20020193304A1
GENERAL INFORMATION:
APPLICANT: WADA, MANABU
APPLICANT: WADA, NAOKO
TITLE OF INVENTION: ANTI-HIV AGENTS

```
FILE REFERENCE: HAYAK-9
CURRENT APPLICATION NUMBER: US/10/076,421
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: JP 2001-42655
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: JP 2001-184284
PRIOR FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
US-10-076-421-2

Query Match      100.0%; Score 44; DB 13; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPSSPPEE 8
Db      156 KPSSPPEE 163

RESULT 18
US-10-171-311-184
Sequence 184, Application US/10171311
Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Glatz, Karen
APPLICANT: Ganavavrapu, Manjula
APPLICANT: Hoersch, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 184
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
US-10-171-311-184

Query Match      100.0%; Score 44; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPSSPPEE 8
Db      156 KPSSPPEE 163

RESULT 19
US-10-193-656-4
Sequence 4, Application US/10193656
Publication No. US20030096733A1
GENERAL INFORMATION:
APPLICANT: NY, Tor
APPLICANT: HOLMDAHL, Rikard
```

```
APPLICANT: Li, Jinao
TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
FILE REFERENCE: 3810/13577-US3
CURRENT APPLICATION NUMBER: US/10/193,656
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/304,461
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/304,490
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/305,182
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: GenBank / P00749
DATABASE ENTRY DATE: 1986-07-21
RELEVANT RESIDUES: (1)..(431)
US-10-193-656-4
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Query Match      100.0%; Score 44; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPSSPPEE 8
Db      156 KPSSPPEE 163
```

```
RESULT 20
US-10-301-822-161
Sequence 161, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPM01-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 161
LENGTH: 431
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-301-822-161
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```
Query Match      100.0%; Score 44; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPSSPPEE 8
Db      156 KPSSPPEE 163
```

RESULT 21
US-10-247-671-149
; Sequence 149, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiftman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; PRIOR FILING DATE: 2002-09-18
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1453334CD1
US-10-247-671-149

Query Match 100.0%; Score 44; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 156 KPSSPPE 163

RESULT 22
US-10-131-985-21
; Sequence 21, Application US/1011985
; Publication No. US20030199440A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Ocleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10351A
; CURRENT APPLICATION NUMBER: US/10/131,985
; PRIOR FILING DATE: 2002-04-25
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-21

Query Match 100.0%; Score 44; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 156 KPSSPPE 163

RESULT 23

US-10-295-027-414
; Sequence 414, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 414
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-414

Query Match 100.0%; Score 44; DB 15; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 156 KPSSPPE 163

RESULT 24
US-10-295-027-1275
; Sequence 1275, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1275
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-1275

Query Match 100.0%; Score 44; DB 15; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 156 KPSSPPEE 163

RESULT 25
US-10-410-962-34
Sequence 34, Application US/10410962
Publication No. US20040077836A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
FILE REFERENCE: 040853-01-5054
CURRENT APPLICATION NUMBER: US/10/410,962
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28

NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
US-10-410-962-34

Query Match 100.0%; Score 44; DB 16; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 156 KPSSPPEE 163

RESULT 26
US-10-411-049-34
Sequence 34, Application US/10411049
Publication No. US20040082026A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
FILE REFERENCE: 040853-01-5055
CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
US-10-411-049-34

Query Match 100.0%; Score 44; DB 16; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 156 KPSSPPEE 163

RESULT 27
US-10-372-966-5
Sequence 56, Application US/10372966
Publication No. US20040111765A1
GENERAL INFORMATION:
APPLICANT: OISHI, Karen K.
APPLICANT: ZHOU, Da-Feng
TITLE OF INVENTION: PRODUCTION OF UROKINASE IN PLANT-BASED EXPRESSION

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; TITLE OF INVENTION: SYSTEMS
; FILE REFERENCE: 048281/0107
; CURRENT APPLICATION NUMBER: US/10/372,966
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: US/09/344,376
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/091,911
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Human and Potato
; US-10-372-966-5

Query Match      100.0%; Score 44; DB 16; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPSSPPE 8
Db      158 KPSSPPE 165

RESULT 28
US-10-087-192-594
; Sequence 594, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 594
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-087-192-594

Query Match      100.0%; Score 44; DB 12; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPSSPPE 8
Db      162 KPSSPPE 169

RESULT 29
US-10-360-101-266
; Sequence 266, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: Patentin version 3.1
```

```

; SEQ ID NO 266
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of urokinase
; US-10-360-101-266

Query Match      100.0%; Score 44; DB 15; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPSSPPE 8
Db      160 KPSSPPE 167

RESULT 30
US-10-235-552-8
; Sequence 8, Application US/10235552
; Publication No. US2003002768A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Terence L.
; TITLE OF INVENTION: ANTI-INVASIVE AND ANTI-ANGIOGENIC COMPOSITIONS AND METHODS
; FILE REFERENCE: 38369-183655
; CURRENT APPLICATION NUMBER: US/10/235,552
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 08/900,327
; PRIOR FILING DATE: 1997-07-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: substitution,
; OTHER INFORMATION: deletion or addition variants of SEQ ID NO:2
; US-10-235-552-8

Query Match      93.2%; Score 41; DB 14; Length 8;
Best Local Similarity 87.5%; Pred. No. 1e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPSSPPE 8
Db      1 RPSSPPE 8

RESULT 31
US-10-235-552-4
; Sequence 4, Application US/10235552
; Publication No. US2003002768A1
; GENERAL INFORMATION:
; APPLICANT: Mazur, Andrew P.
; APPLICANT: Jones, Terence L.
; TITLE OF INVENTION: ANTI-INVASIVE AND ANTI-ANGIOGENIC COMPOSITIONS AND METHODS
; FILE REFERENCE: 38369-183655
; CURRENT APPLICATION NUMBER: US/10/235,552
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 08/900,327
; PRIOR FILING DATE: 1997-07-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: substitution,
; OTHER INFORMATION: deletion or addition variants of SEQ ID NO:2
; FEATURE:
```

NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)
OTHER INFORMATION: AMIDATION
US-10-235-552-4

Query Match 88.6%; Score 39; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSSPPE 8
Db 1 PSSPPE 7

RESULT 32
US-10-235-552-5
Sequence 5, Application US/10235552
Publication No. US20030027768A1
GENERAL INFORMATION:
APPLICANT: Mazar, Andrew P.
APPLICANT: Jones, Terence L.
TITLE OF INVENTION: ANTI-INVASIVE AND ANTI-ANGIOGENIC COMPOSITIONS AND METHODS
FILE REFERENCE: 38369-183655
CURRENT APPLICATION NUMBER: US/10/235,552
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 08/900,327
PRIOR FILING DATE: 1997-07-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: substitution,
OTHER INFORMATION: deletion or addition variants of SEQ ID NO:2
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)
OTHER INFORMATION: AMIDATION
US-10-235-552-5

Query Match 88.6%; Score 39; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 7
Db 1 KPSSPPE 7

RESULT 33
US-10-235-552-6
Sequence 6, Application US/10235552
Publication No. US20030027768A1
GENERAL INFORMATION:
APPLICANT: Mazar, Andrew P.
APPLICANT: Jones, Terence L.
TITLE OF INVENTION: ANTI-INVASIVE AND ANTI-ANGIOGENIC COMPOSITIONS AND METHODS
FILE REFERENCE: 38369-183655
CURRENT APPLICATION NUMBER: US/10/235,552
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 08/900,327
PRIOR FILING DATE: 1997-07-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: substitution,
OTHER INFORMATION: deletion or addition variants of SEQ ID NO:2
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)
OTHER INFORMATION: AMIDATION
US-10-235-552-6

Query Match 88.6%; Score 39; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 7
Db 1 KPSSPPE 7

RESULT 34
US-10-235-552-7
Sequence 7, Application US/10235552
Publication No. US20030027768A1
GENERAL INFORMATION:
APPLICANT: Mazar, Andrew P.
APPLICANT: Jones, Terence L.
TITLE OF INVENTION: ANTI-INVASIVE AND ANTI-ANGIOGENIC COMPOSITIONS AND METHODS
FILE REFERENCE: 38369-183655
CURRENT APPLICATION NUMBER: US/10/235,552
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 08/900,327
PRIOR FILING DATE: 1997-07-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: substitution,
OTHER INFORMATION: deletion or addition variants of SEQ ID NO:2
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: AMIDATION
US-10-235-552-7

Query Match 86.4%; Score 38; DB 14; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 1 KPSSPPE 8

RESULT 35
US-09-864-761-37883
Sequence 37883, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: substitution,
OTHER INFORMATION: deletion or addition variants of SEQ ID NO:2
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: AMIDATION
US-10-235-552-7

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: substitution,
OTHER INFORMATION: deletion or addition variants of SEQ ID NO:2
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: AMIDATION
US-10-235-552-6

Query Match 86.4%; Score 38; DB 14; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 1 KPSSPPE 8

RESULT 34
US-10-235-552-7
Sequence 7, Application US/10235552
Publication No. US20030027768A1
GENERAL INFORMATION:
APPLICANT: Mazar, Andrew P.
APPLICANT: Jones, Terence L.
TITLE OF INVENTION: ANTI-INVASIVE AND ANTI-ANGIOGENIC COMPOSITIONS AND METHODS
FILE REFERENCE: 38369-183655
CURRENT APPLICATION NUMBER: US/10/235,552
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 08/900,327
PRIOR FILING DATE: 1997-07-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: substitution,
OTHER INFORMATION: deletion or addition variants of SEQ ID NO:2
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: AMIDATION
US-10-235-552-7

Query Match 86.4%; Score 38; DB 14; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 1 KPSSPPE 8

RESULT 35
US-09-864-761-37883
Sequence 37883, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: substitution,
OTHER INFORMATION: deletion or addition variants of SEQ ID NO:2
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: AMIDATION
US-10-235-552-7

Query Match 86.4%; Score 38; DB 14; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 1 KPSSPPE 8

RESULT 35
US-09-864-761-37883
Sequence 37883, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: substitution,
OTHER INFORMATION: deletion or addition variants of SEQ ID NO:2
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: AMIDATION
US-10-235-552-7

APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 37883
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC011232.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
OTHER INFORMATION: EST HUMAN HIT: AM444637.1, EVALUE 1.00e-76
OTHER INFORMATION: SWISSPROT HIT: Q9ZHB3, EVALUE 2.80e+00
US-09-864-761-37883

Query Match 86.4%; Score 38; DB 9; Length 166;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
1 KPSSPPE 8
|||||

Db 84 KPSSPPE 91
RESULT 36
US-09-864-761-46504
Sequence 46504, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 46504
LENGTH: 166
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL121653.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.92
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EST HUMAN HIT: AM444637.1, EVALUE 1.00e-76
OTHER INFORMATION: SWISSPROT HIT: Q9ZHB3, EVALUE 2.80e+00
US-09-864-761-46504

Query Match 86.4%; Score 38; DB 9; Length 166;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 84 KPSSPPEE 91

RESULT 37
US-10-108-260A-3871

Sequence 3871, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3871
LENGTH: 264
TYPE: PRT
ORGANISM: Homo sapiens
US-10-108-260A-3871

Query Match 86.4%; Score 38; DB 15; Length 264;
Best Local Similarity 87.5%; Pred. No. 6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 182 KPSSPPEE 189

RESULT 38
US-10-176-306-23

Sequence 23, Application US/10176306
Publication No. US20030130485A1
GENERAL INFORMATION:
APPLICANT: Meyers, Rachel A.
APPLICANT: Curtis, Rory A. J.
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Bandaru, Rajasekhar
APPLICANT: Kapeller-Liebermann, Rosana
TITLE OF INVENTION: NOVEL HUMAN GENES AND METHODS OF USE THEREOF
FILE REFERENCE: 10448-195001
CURRENT APPLICATION NUMBER: US/10/176,306
CURRENT FILING DATE: 2002-06-20
PRIOR APPLICATION NUMBER: 10/001,137
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: PCT/US01/45291
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/248,362
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: 60/248,331
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: 60/248,365
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: 60/250,077
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/250,327
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/250,176
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 10/023,617
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: PCT/US01/49416
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 60/256,249
PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/256,405

PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 10/083,248
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: PCT/US01/46717
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/242,324
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/242,518
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/241,989
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-10-176-306-23

Qy 1 KPSSPPEE 8
Db 379 KPSSPPEE 386

RESULT 39
US-10-094-749-2145

Sequence 2145, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOHYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2145
LENGTH: 461
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2145

Query Match 86.4%; Score 38; DB 15; Length 461;
Best Local Similarity 87.5%; Pred. No. 1e+03;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 182 KPSSPPEE 189

Db 379 KPSSPPE 386

RESULT 40

US-10-295-027-205

Sequence 205, Application US/10295027

Publication No. US2003023350A1

GENERAL INFORMATION:

APPLICANT: Afar, Daniel

APPLICANT: Aziz, Natasha

APPLICANT: Ginsberg, Wendy M.

APPLICANT: Gish, Kurt C.

APPLICANT: Glynn, Richard

APPLICANT: Hevizi, Peter A.

APPLICANT: Mack, David H.

APPLICANT: Murray, Richard

APPLICANT: Watson, Susan R.

APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

FILE REFERENCE: 018501-012500US

CURRENT FILING DATE: 2002-11-13

PRIOR FILING DATE: 2000-09-15

PRIOR FILING DATE: 2000-09-15

PRIOR FILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-11-15

PRIOR FILING DATE: 2001-11-15

PRIOR FILING DATE: 2001-11-21

PRIOR FILING DATE: 2001-11-29

PRIOR FILING DATE: 2001-12-14

PRIOR FILING DATE: 2002-01-08

PRIOR FILING DATE: 2002-01-10

PRIOR FILING DATE: 2002-02-08

PRIOR FILING DATE: 2002-02-13

PRIOR FILING DATE: 2002-02-13

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 1386

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 205

LENGTH: 461

TYPE: PRT

ORGANISM: Homo sapiens

US-10-295-027-205

Query Match 86.4%; Score 38; DB 15; Length 461;

Best Local Similarity 87.5%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSSPPE 8

Db 379 KPSSPPE 386

RESULT 41

US-10-188-832-97

Sequence 97, Application US/10188832

Publication No. US20040076955A1

GENERAL INFORMATION:

APPLICANT: Mack, David H.

APPLICANT: Aziz, Natasha

APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions

TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder

FILE REFERENCE: 018501-002330US

CURRENT APPLICATION NUMBER: US/10/188,832

CURRENT FILING DATE: 2002-11-22

PRIOR APPLICATION NUMBER: US 60/302,814

PRIOR FILING DATE: 2001-07-03

PRIOR APPLICATION NUMBER: US 60/310,099

PRIOR FILING DATE: 2001-08-03

PRIOR APPLICATION NUMBER: US 60/343,705

PRIOR FILING DATE: 2001-11-08

PRIOR APPLICATION NUMBER: US 60/350,666

PRIOR FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 60/372,246

PRIOR FILING DATE: 2002-04-12

NUMBER OF SEQ ID NOS: 207

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 97

LENGTH: 461

TYPE: PRT

ORGANISM: Homo sapiens

US-10-188-832-97

QY 1 KPSSPPE 8

Db 379 KPSSPPE 386

RESULT 42

US-09-972-035A-20

Sequence 20, Application US/09972035A

Patent No. US20020173622A1

GENERAL INFORMATION:

APPLICANT: Wettstein, Daniel A

APPLICANT: Morham, Scott

APPLICANT: Zavitz, Kenton

TITLE OF INVENTION: Tsg101-GAGp6 INTERACTION AND USE THEREOF

FILE REFERENCE: 1907.03

CURRENT APPLICATION NUMBER: US/09/972,035A

CURRENT FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: US 60/276,259

PRIOR FILING DATE: 2001-03-14

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn version 3.1

SEQ ID NO 20

LENGTH: 8

TYPE: PRT

ORGANISM: Human immunodeficiency virus

US-09-972-035A-20

QY 1 KPSSPPE 8

Db 1 EPSAPPE 8

RESULT 43

US-10-223-172A-20

Sequence 20, Application US/10223172A

Publication No. US2003018444A1

GENERAL INFORMATION:

APPLICANT: Myriad Genetics, Inc.

APPLICANT: Zavitz, Kenton

APPLICANT: Wettstein, Daniel Albert

APPLICANT: Morham, Scott

APPLICANT: Hobden, Adrian

TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING HIV INFECTION

FILE REFERENCE: 5003.01

CURRENT APPLICATION NUMBER: US/10/223,172A

CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/313,239
PRIOR FILING DATE: 2001-08-18
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 8
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-10-223-172A-20

Query Match
Best Local Similarity 84.1%; Score 37; DB 14; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
Db 1 EPSAPPEE 8

RESULT 44
US-10-224-999A-20
Sequence 20, Application US/10224999A
Publication No. US20030171318A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection
FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484
SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 8
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-10-224-999A-20

Query Match
Best Local Similarity 84.1%; Score 37; DB 14; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
Db 1 EPSAPPEE 8

RESULT 45
US-10-663-407-20
Sequence 20, Application US/10663407
Publication No. US20040109861A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Incorporated
APPLICANT: Wetstein, Daniel A
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
TITLE OF INVENTION: TSG101-GAG INTERACTION AND USE THEREOF
FILE REFERENCE: 1907.04-1
CURRENT APPLICATION NUMBER: US/10/663,407
CURRENT FILING DATE: 2003-09-15
PRIOR APPLICATION NUMBER: PCT/US02/08146
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: US 10/223,172
PRIOR FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 10/224,999
PRIOR FILING DATE: 2002-08-20
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.2

SEQ ID NO 20
LENGTH: 8
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-10-663-407-20

Query Match
Best Local Similarity 84.1%; Score 37; DB 16; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
Db 1 EPSAPPEE 8

RESULT 46
US-09-972-035A-24
Sequence 24, Application US/09972035A
Patent No. US20020173622A1
GENERAL INFORMATION:
APPLICANT: Wetstein, Daniel A
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
TITLE OF INVENTION: TSG101-GAGp6 INTERACTION AND USE THEREOF
FILE REFERENCE: 1907.03
CURRENT APPLICATION NUMBER: US/09/972,035A
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: US 60/276,259
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 9
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-09-972-035A-24

Query Match
Best Local Similarity 84.1%; Score 37; DB 9; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
Db 2 EPSAPPEE 9

RESULT 47
US-10-223-172A-24
Sequence 24, Application US/10223172A
Publication No. US20030138444A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Zavitz, Kenton
APPLICANT: Wetstein, Daniel Albert
APPLICANT: Morham, Scott
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: COMPOSITION AND METHOD FOR TREATING HIV INFECTION
FILE REFERENCE: 5003.01
CURRENT APPLICATION NUMBER: US/10/223,172A
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/313,239
PRIOR FILING DATE: 2001-08-18
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 9
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-10-223-172A-24

Query Match
Best Local Similarity 84.1%; Score 37; DB 14; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
:|:|:|
Db 2 EPSAPPEE 9

RESULT 48

US-10-224-999A-24
; Sequence 24, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-224-999A-24

Query Match 84.1%; Score 37; DB 14; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
:|:|:|
Db 2 EPSAPPEE 9

RESULT 49

US-10-663-407-24
; Sequence 24, Application US/10663407
; Publication No. US20040109861A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Incorporated
; APPLICANT: Wettstein, Daniel A
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; TITLE OF INVENTION: TSG101-GAG INTERACTION AND USE THEREOF
; FILE REFERENCE: 1907.04-1
; CURRENT APPLICATION NUMBER: US/10/663,407
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: PCT/US02/08146
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: US 10/223,172
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 10/224,999
; PRIOR FILING DATE: 2002-08-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-663-407-24

Query Match 84.1%; Score 37; DB 16; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
:|:|:|
Db 2 EPSAPPEE 9

RESULT 50
US-09-972-035A-26
; Sequence 26, Application US/09972035A
; Patent No. US20020173622A1
; GENERAL INFORMATION:
; APPLICANT: Wettstein, Daniel A
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; TITLE OF INVENTION: Tsg101-GAGp6 INTERACTION AND USE THEREOF
; FILE REFERENCE: 1907.03
; CURRENT APPLICATION NUMBER: US/09/972,035A
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/276,259
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-972-035A-26

Query Match 84.1%; Score 37; DB 9; Length 10;
Best Local Similarity 75.0%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
:|:|:|
Db 3 EPSAPPEE 10

Search completed: June 18, 2004, 13:01:57
Job time : 49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2004, 12:52:03 ; Search time 55 Seconds
(without alignments)
41.098 Million cell updates/sec

Title: US-10-655-201-2

Perfect score: 44

Sequence: 1 KPSPPEE 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 500 summaries

Database : A_Geneseq.29yan04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	8	AAW95057	AAW95057 Anti-inva
2	44	100.0	8	AB882274	Abb82274 Tumour an
3	44	100.0	8	AB882273	Abb82273 Peptide c
4	44	100.0	8	ADC66464	ADC66464 Human utro
5	44	100.0	9	AAW95058	AAW95058 Urokinase
6	44	100.0	10	AAW95056	AAW95056 Urokinase
7	44	100.0	10	AB882272	Abb82272 Plasminog
8	44	100.0	10	ADC66463	ADC66463 Human utro
9	44	100.0	21	AAE81672	AAE81672 Sequence
10	44	100.0	21	AAW22737	AAW22737 Linking s
11	44	100.0	96	AAE16550	AAE16550 Human uPA
12	44	100.0	143	AAE16549	AAE16549 Human uPA
13	44	100.0	208	AAW22747	AAW22747 Metastasi
14	44	100.0	259	AAE63140	AAE63140 Low molec
15	44	100.0	276	AAE16546	AAE16546 Human LMW
16	44	100.0	323	AAE16548	AAE16548 Human uPA
17	44	100.0	337	AAE16549	AAE16549 Human uPA
18	44	100.0	337	ABP41795	ABP41795 Human ova
19	44	100.0	365	AAE68854	AAE68854 Delta 1-4
20	44	100.0	378	AAW13635	AAW13635 Human pro
21	44	100.0	386	AAE66266	AAE66266 Bifunctio
22	44	100.0	389	AAW13636	AAW13636 Human pro
23	44	100.0	390	AAE66245	AAE66245 Bifunctio
24	44	100.0	390	AAE66247	AAE66247 Bifunctio
25	44	100.0	392	AAE66260	AAE66260 Bifunctio

26	44	100.0	392	2	AAE66264	AAE66264 Bifunctio
27	44	100.0	392	2	AAE66255	AAE66255 Bifunctio
28	44	100.0	392	2	AAE66259	AAE66259 Bifunctio
29	44	100.0	392	2	AAE66261	AAE66261 Bifunctio
30	44	100.0	392	2	AAE66258	AAE66258 Bifunctio
31	44	100.0	392	2	AAE66263	AAE66263 Bifunctio
32	44	100.0	392	2	AAE66254	AAE66254 Bifunctio
33	44	100.0	392	2	AAE66256	AAE66256 Bifunctio
34	44	100.0	392	2	AAE66257	AAE66257 Bifunctio
35	44	100.0	393	2	AAE66251	AAE66251 Bifunctio
36	44	100.0	393	2	AAE66253	AAE66253 Bifunctio
37	44	100.0	393	2	AAE66249	AAE66249 Bifunctio
38	44	100.0	393	2	AAE66252	AAE66252 Bifunctio
39	44	100.0	393	2	AAE66244	AAE66244 Bifunctio
40	44	100.0	393	2	AAE66250	AAE66250 Bifunctio
41	44	100.0	393	2	AAE99597	AAE99597 Chimeric
42	44	100.0	393	2	AAE99596	AAE99596 Chimeric
43	44	100.0	393	2	AAE99885	AAE99885 M36: fibr
44	44	100.0	395	2	AAE47902	AAE47902 Pro-uroki
45	44	100.0	395	2	AAE66265	AAE66265 Bifunctio
46	44	100.0	395	2	AAE66262	AAE66262 Bifunctio
47	44	100.0	396	2	AAE66246	AAE66246 Bifunctio
48	44	100.0	397	2	AAE11828	AAE11828 FB-FB-UK
49	44	100.0	397	2	AAE66248	AAE66248 Bifunctio
50	44	100.0	401	2	AAW13637	AAW13637 Human pro
51	44	100.0	410	2	AAE23794	AAE23794 Prourokin
52	44	100.0	411	1	AAE50871	AAE50871 Sequence
53	44	100.0	411	1	AAE91684	AAE91684 Sequence
54	44	100.0	411	1	AAE96146	AAE96146 Sequence
55	44	100.0	411	1	AAE93589	AAE93589 Amino aci
56	44	100.0	411	1	AAE93504	AAE93504 Sequence
57	44	100.0	411	2	AAE66244	AAE66244 Urokinase
58	44	100.0	411	2	AAE07904	AAE07904 Human pro
59	44	100.0	411	2	AAE07902	AAE07902 Human pro
60	44	100.0	411	2	AAE07903	AAE07903 Human pro
61	44	100.0	411	2	AAE05117	AAE05117 UK-S3 as
62	44	100.0	411	2	AAW13634	AAW13634 Human nat
63	44	100.0	411	2	AAE10057	AAE10057 Pro-uroki
64	44	100.0	411	2	AAE10058	AAE10058 Pro-uroki
65	44	100.0	411	2	AAE10056	AAE10056 Pro-uroki
66	44	100.0	411	2	AAE22098	AAE22098 Pro-UK, 3
67	44	100.0	411	2	AAE34584	AAE34584 Mutant hu
68	44	100.0	411	2	AAE47956	AAE47956 PUK G16A
69	44	100.0	411	2	AAE47966	AAE47966 PUK G16A
70	44	100.0	411	2	AAE47962	AAE47962 PUK G38A
71	44	100.0	411	2	AAE47963	AAE47963 PUK G53A
72	44	100.0	411	2	AAE40225	AAE40225 PUK, 2/19
73	44	100.0	411	2	AAE47965	AAE47965 PUK N32P
74	44	100.0	411	2	AAE47958	AAE47958 PUK S26T
75	44	100.0	411	2	AAE47961	AAE47961 PUK G38A
76	44	100.0	411	2	AAE47959	AAE47959 PUK G32P
77	44	100.0	411	2	AAE47960	AAE47960 PUK P34A
78	44	100.0	411	2	AAE47964	AAE47964 PUK N32P
79	44	100.0	411	2	AAE47957	AAE47957 PUK Y24A
80	44	100.0	411	2	AAE62997	AAE62997 Pro-uroki
81	44	100.0	411	2	AAE63008	AAE63008 Pro-uroki
82	44	100.0	411	2	AAE62989	AAE62989 Pro-uroki
83	44	100.0	411	2	AAE62994	AAE62994 Pro-uroki
84	44	100.0	411	2	AAE63003	AAE63003 Pro-uroki
85	44	100.0	411	2	AAE63001	AAE63001 Pro-uroki
86	44	100.0	411	2	AAE63006	AAE63006 Pro-uroki
87	44	100.0	411	2	AAE62992	AAE62992 Pro-uroki
88	44	100.0	411	2	AAE63002	AAE63002 Pro-uroki
89	44	100.0	411	2	AAE63007	AAE63007 Pro-uroki
90	44	100.0	411	2	AAE62995	AAE62995 Pro-uroki
91	44	100.0	411	2	AAE63000	AAE63000 Pro-uroki
92	44	100.0	411	2	AAE63004	AAE63004 Pro-uroki
93	44	100.0	411	2	AAE62996	AAE62996 Pro-uroki
94	44	100.0	411	2	AAE63005	AAE63005 Pro-uroki
95	44	100.0	411	2	AAE62991	AAE62991 Pro-uroki
96	44	100.0	411	2	AAE62998	AAE62998 Pro-uroki
97	44	100.0	411	2	AAE62993	AAE62993 Pro-uroki
98	44	100.0	411	2	AAE92926	AAE92926 Pro-uroki

99	44	100.0	411	2	AAW19709	AAW19709	Pro-uroki	172	44	100.0	434	2	AAW20537	AAW20537	Amidated
100	44	100.0	411	2	AAW39343	AAW39343	Human pro	173	44	100.0	434	2	AAW20538	AAW20538	Amidated
101	44	100.0	411	2	AAW42284	AAW42284	Human pro	174	44	100.0	436	2	AAW20536	AAW20536	Amidated
102	44	100.0	411	3	AAW92836	AAW92836	Urokinase	175	44	100.0	473	1	AAW60797	AAW60797	Interfero
103	44	100.0	411	3	AAW78343	AAW78343	Human pro	176	41	93.2	8	2	AAW95052	AAW95052	Urokinase
104	44	100.0	411	4	AAW20489	AAW20489	Human pro	177	41	93.2	8	2	AAW82277	AAW82277	Urokinase
105	44	100.0	411	4	AAW74797	AAW74797	Human pro	178	41	93.2	8	7	ADCC6470	ADCC6470	Human uro
106	44	100.0	411	5	AAW16544	AAW16544	Human uro	179	40	90.9	380	2	AAW05433	AAW05433	CPA-P2 Hy
107	44	100.0	411	5	AAW13269	AAW13269	Human pro	180	40	90.9	410	2	AAW23795	AAW23795	Prourokin
108	44	100.0	411	7	ADCC72159	ADCC72159	Human uro	181	39	88.6	7	2	AAW95063	AAW95063	Urokinase
109	44	100.0	411	7	ADCC85977	ADCC85977	Human uro	182	39	88.6	7	2	AAW95054	AAW95054	Urokinase
110	44	100.0	412	2	AAW10334	AAW10334	Human uro	183	39	88.6	7	2	AAW82279	AAW82279	Urokinase
111	44	100.0	421	2	AAW10173	AAW10173	Human pro	184	39	88.6	7	5	AAW82278	AAW82278	Urokinase
112	44	100.0	421	2	AAW10172	AAW10172	Human pro	185	39	88.6	7	7	ADCC6467	ADCC6467	Human uro
113	44	100.0	424	2	AAW24579	AAW24579	Inhibitor	186	39	88.6	7	7	ADCC6466	ADCC6466	Human uro
114	44	100.0	425	2	AAW10171	AAW10171	Human pro	187	39	88.6	8	7	ADCC6472	ADCC6472	Human uro
115	44	100.0	430	2	AAW24578	AAW24578	Inhibitor	188	39	88.6	11	2	AAW95059	AAW95059	Urokinase
116	44	100.0	430	3	AAW78341	AAW78341	Human pro	189	39	88.6	11	2	AAW82280	AAW82280	Urokinase
117	44	100.0	431	1	AAW30041	AAW30041	Sequence	190	39	88.6	27	2	AAW05105	AAW05105	Plasminog
118	44	100.0	431	1	AAW50503	AAW50503	Sequence	191	39	88.6	380	2	AAW22504	AAW22504	[GARSQ] -
119	44	100.0	431	1	AAW50114	AAW50114	Sequence	192	39	88.6	411	1	AAW80428	AAW80428	Sequence
120	44	100.0	431	1	AAW60783	AAW60783	Human uro	193	39	88.6	411	2	AAW04185	AAW04185	Plasminog
121	44	100.0	431	1	AAW60674	AAW60674	Modified	194	39	88.6	476	2	AAW22503	AAW22503	[GARSQ] -
122	44	100.0	431	1	AAW70258	AAW70258	Sequence	195	39	88.6	919	4	AAW07234	AAW07234	Novel hum
123	44	100.0	431	1	AAW71491	AAW71491	Modified	196	39	88.6	1178	7	ADCC6838	ADCC6838	Letuce E
124	44	100.0	431	1	AAW71663	AAW71663	Modified	197	38	86.4	8	2	AAW95061	AAW95061	Urokinase
125	44	100.0	431	1	AAW71698	AAW71698	Modified	198	38	86.4	8	2	AAW95060	AAW95060	Urokinase
126	44	100.0	431	1	AAW71699	AAW71699	Modified	199	38	86.4	8	5	AAW82276	AAW82276	Urokinase
127	44	100.0	431	1	AAW70250	AAW70250	Sequence	200	38	86.4	8	5	AAW82275	AAW82275	Urokinase
128	44	100.0	431	1	AAW80430	AAW80430	Deduced A	201	38	86.4	8	7	ADCC6469	ADCC6469	Human uro
129	44	100.0	431	1	AAW81204	AAW81204	Pro-uroki	202	38	86.4	166	4	ADCC6468	ADCC6468	Human uro
130	44	100.0	431	1	AAW91886	AAW91886	Sequence	203	38	86.4	166	4	AAW18264	AAW18264	Peptide #
131	44	100.0	431	1	AAW92119	AAW92119	Natural h	204	38	86.4	166	4	AAW15177	AAW15177	Peptide #
132	44	100.0	431	1	AAW94764	AAW94764	Non-glyco	205	38	86.4	166	4	AAW34170	AAW34170	Peptide #
133	44	100.0	431	2	AAW07112	AAW07112	Human pro	206	38	86.4	166	4	AAW37296	AAW37296	Peptide #
134	44	100.0	431	2	AAW04253	AAW04253	Human pro	207	38	86.4	166	4	AAW7634	AAW7634	Peptide #
135	44	100.0	431	2	AAW63141	AAW63141	Full leng	208	38	86.4	166	4	AAW30756	AAW30756	Peptide #
136	44	100.0	431	2	AAW47903	AAW47903	Pro-uroki	209	38	86.4	166	4	AAW32047	AAW32047	Peptide #
137	44	100.0	431	2	AAW33199	AAW33199	Human uro	210	38	86.4	166	4	AAW82585	AAW82585	Protein #
138	44	100.0	431	2	AAW33198	AAW33198	Human uro	211	38	86.4	166	4	AAW67343	AAW67343	Human bon
139	44	100.0	431	2	AAW33121	AAW33121	Human uro	212	38	86.4	166	4	AAW70434	AAW70434	Human bon
140	44	100.0	431	3	AAW50865	AAW50865	Human uro	213	38	86.4	166	4	AAW57998	AAW57998	Human bon
141	44	100.0	431	3	AAW99591	AAW99591	Human pro	214	38	86.4	166	4	AAW49006	AAW49006	Human bon
142	44	100.0	431	3	AAW84605	AAW84605	Human pro	215	38	86.4	166	4	AAW52114	AAW52114	Human bon
143	44	100.0	431	5	AAW17128	AAW17128	Human uro	216	38	86.4	166	4	AAW05878	AAW05878	Peptide #
144	44	100.0	431	5	AAW99232	AAW99232	Human uro	217	38	86.4	166	4	AAW05878	AAW05878	Peptide #
145	44	100.0	431	5	AAW99228	AAW99228	Human pro	218	38	86.4	166	4	AAW02915	AAW02915	Peptide #
146	44	100.0	431	5	AAW99237	AAW99237	Human pro	219	38	86.4	166	4	AAW40068	AAW40068	Human pep
147	44	100.0	431	5	AAW99242	AAW99242	Human pro	220	38	86.4	166	5	AAW36981	AAW36981	Human pep
148	44	100.0	431	5	AAW99240	AAW99240	Human pro	221	38	86.4	166	5	AAW98525	AAW98525	Zinc iron
149	44	100.0	431	5	AAW99238	AAW99238	Human pro	222	38	86.4	461	5	AAW99908	AAW99908	Human 647
150	44	100.0	431	5	AAW99231	AAW99231	Human pro	223	38	86.4	461	6	ADW4577	ADW4577	Human pro
151	44	100.0	431	5	AAW99229	AAW99229	Human pro	224	38	86.4	461	6	AAW48190	AAW48190	Human pro
152	44	100.0	431	5	AAW99230	AAW99230	Human pro	225	38	86.4	461	6	AAW56642	AAW56642	Human pro
153	44	100.0	431	5	AAW99234	AAW99234	Human pro	226	38	86.4	477	6	AAW08221	AAW08221	Novel hum
154	44	100.0	431	5	AAW99239	AAW99239	Human pro	227	38	86.4	477	6	AAW54774	AAW54774	Peptide 1
155	44	100.0	431	5	AAW99243	AAW99243	Human pro	228	37	84.1	8	6	AAW96521	AAW96521	Human pro
156	44	100.0	431	5	AAW99233	AAW99233	Human pro	229	37	84.1	8	6	AAW82413	AAW82413	Human pro
157	44	100.0	431	5	AAW99235	AAW99235	Human pro	230	37	84.1	9	5	AAW96525	AAW96525	Human pro
158	44	100.0	431	5	AAW99236	AAW99236	Human pro	231	37	84.1	9	6	AAW82417	AAW82417	Human pro
159	44	100.0	431	5	AAW99241	AAW99241	Human pro	232	37	84.1	9	6	AAW82417	AAW82417	Human pro
160	44	100.0	431	5	AAW99240	AAW99240	Human pro	233	37	84.1	10	5	AAW96530	AAW96530	Human pro
161	44	100.0	431	6	AAW37128	AAW37128	Human uro	234	37	84.1	10	6	AAW96530	AAW96530	Human pro
162	44	100.0	431	6	AAW55855	AAW55855	Human uro	235	37	84.1	10	6	AAW82419	AAW82419	Human pro
163	44	100.0	431	6	AAW56547	AAW56547	Human uro	236	37	84.1	13	5	AAW54784	AAW54784	Human pro
164	44	100.0	431	6	AAW56708	AAW56708	Lung cano	237	37	84.1	13	6	AAW96538	AAW96538	Human pro
165	44	100.0	431	6	AAW11076	AAW11076	Human uro	238	37	84.1	13	6	AAW82423	AAW82423	Human pro
166	44	100.0	431	6	AAW92137	AAW92137	Human cer	239	37	84.1	14	5	AAW54786	AAW54786	Peptide 1
167	44	100.0	431	7	AAW46429	AAW46429	Human pro	240	37	84.1	14	6	AAW82425	AAW82425	Human pro
168	44	100.0	431	7	AAW325745	AAW325745	Human pro	241	37	84.1	202	4	AAW61097	AAW61097	Human pro
169	44	100.0	431	7	AAW43393	AAW43393	Human uro	242	37	84.1	1099	4	AAW68903	AAW68903	Human pro
170	44	100.0	432	2	AAW99888	AAW99888	W3: fibr	243	37	84.1	1151	1	AAW61598	AAW61598	Drosophi
171	44	100.0	433	3	AAW78342	AAW78342	Patatin s	244	36	81.8	9	6	AAW96528	AAW96528	Human pro

245	36	81.8	10	6	ABP6534	Abp6534	HIV	GAG	P	318	36	81.8	1089	6	ABR59317	Abt59317	Human	sec
246	36	81.8	56	2	AA74180	Aa74180	Human	pro		319	36	81.8	1089	6	ABO09379	AbO09379	Human	sec
247	36	81.8	56	2	AA74400	Aa74400	Human	pro		320	36	81.8	1089	6	ABO19243	AbO19243	Novel	hum
248	36	81.8	84	6	ABR58380	Abt58380	Human	NOV		321	36	81.8	1089	6	ABO11261	AbO11261	Human	sec
249	36	81.8	111	3	AAO3717	AaO3717	Human	sec		322	36	81.8	1089	6	ABR66879	Abt66879	Human	sec
250	36	81.8	134	4	AAO10357	AaO10357	Human	pol		323	36	81.8	1089	6	ABO16092	AbO16092	Human	sec
251	36	81.8	263	4	ABR60326	Abb60326	Drosophila			324	36	81.8	1089	6	ABO13798	AbO13798	Human	sec
252	36	81.8	362	2	AAW97364	Aaw97364	Amino	act		325	36	81.8	1089	6	ABU65701	Abu65701	Human	sec
253	36	81.8	362	4	AAE10305	Aae10305	Human	pig		326	36	81.8	1089	6	ABO07549	AbO07549	Human	PRO
254	36	81.8	362	4	AAU08652	Aau08652	Human	ant		327	36	81.8	1089	6	ABO03736	AbO03736	Human	sec
255	36	81.8	362	5	ABR08433	Abb08433	SLED	poly		328	36	81.8	1089	6	ABR67184	Abt67184	Human	sec
256	36	81.8	362	5	ABR04587	Abb04587	Human	ant		329	36	81.8	1089	6	ABO15787	AbO15787	Human	sec
257	36	81.8	411	5	AAE16551	Aae16551	Human	uro		330	36	81.8	1089	6	ABU56068	Abu56068	Human	sec
258	36	81.8	418	2	AAE4800	Aae4800	Sequence			331	36	81.8	1089	6	ABU55396	Abu55396	Human	PRO
259	36	81.8	418	2	AAE90287	Aae90287	Pigment	e		332	36	81.8	1089	6	ABU95341	Abu95341	Novel	hum
260	36	81.8	418	4	AAE10306	Aae10306	Human	pig		333	36	81.8	1089	6	ABU71244	Abu71244	Human	PRO
261	36	81.8	418	5	ABR81091	Abb81091	Human	pig		334	36	81.8	1089	6	ABO07854	AbO07854	Human	PRO
262	36	81.8	418	6	ABR58379	Abt58379	Human	NOV		335	36	81.8	1089	6	ABR70095	Abt70095	Human	sec
263	36	81.8	418	6	ABR58379	Abt58379	Human	NOV		336	36	81.8	1089	6	ABR69428	Abt69428	Human	sec
264	36	81.8	418	6	AAE38136	Aae38136	Human	ret		337	36	81.8	1089	6	ABO01569	AbO01569	Human	PRO
265	36	81.8	418	7	ABU10031	Abu10031	Human	pig		338	36	81.8	1089	6	ABU81371	Abu81371	Human	PRO
266	36	81.8	418	7	ABR59089	Abb59089	Human	ret		339	36	81.8	1089	6	ABR60168	Abt60168	Human	sec
267	36	81.8	494	4	ABR70259	Abb70259	Drosophila			340	36	81.8	1089	6	ABR67903	Abt67903	Human	sec
268	36	81.8	574	3	AAE33227	Aae33227	Human	pro		341	36	81.8	1089	6	ABR65291	Abt65291	Human	sec
269	36	81.8	671	3	AAE24257	Aae24257	Arabidops			342	36	81.8	1089	6	ABR68513	Abt68513	Human	sec
270	36	81.8	671	4	AAU00463	Aau00463	Arabidops			343	36	81.8	1089	6	ABR71925	Abt71925	Human	PRO
271	36	81.8	672	6	AAE37052	Aae37052	Human	gen		344	36	81.8	1089	6	ABU85405	Abu85405	Human	PRO
272	36	81.8	672	6	AAE37066	Aae37066	Human	gen		345	36	81.8	1089	6	ABU89095	Abu89095	Human	sec
273	36	81.8	672	6	AAE37276	Aae37276	Human	gen		346	36	81.8	1089	6	ABU83175	Abu83175	Human	sec
274	36	81.8	747	4	AAE84251	Aae84251	Human	cyt		347	36	81.8	1089	6	ABU95031	Abu95031	Novel	hum
275	36	81.8	851	7	ADCE4335	Adce4335	KIRA1196			348	36	81.8	1089	6	ABU90579	Abu90579	Novel	hum
276	36	81.8	880	7	ADD14150	Add14150	Human	src		349	36	81.8	1089	6	ABU84090	Abu84090	Human	sec
277	36	81.8	896	4	AAW44252	Aaw44252	Human	EST		350	36	81.8	1089	6	ABU93741	Abu93741	Novel	hum
278	36	81.8	988	4	AAE84252	Aae84252	Amino	act		351	36	81.8	1089	6	ABR64986	Abt64986	Human	sec
279	36	81.8	1089	3	AAE93369	Aae93369	Human	PRO		352	36	81.8	1089	6	ABR68818	Abt68818	Human	sec
280	36	81.8	1089	4	AAE66118	Aae66118	Protein	O		353	36	81.8	1089	6	ABO06634	AbO06634	Human	sec
281	36	81.8	1089	4	AAU29156	Aau29156	Human	PRO		354	36	81.8	1089	6	ABR99179	Abt99179	Human	sec
282	36	81.8	1089	6	ABU85532	Abu85532	Human	PRO		355	36	81.8	1089	6	ABU57063	Abu57063	Human	PRO
283	36	81.8	1089	6	ABU88080	Abu88080	Novel	hum		356	36	81.8	1089	6	ABU86015	Abu86015	Novel	hum
284	36	81.8	1089	6	ABU84395	Abu84395	Human	sec		357	36	81.8	1089	6	ABU82302	Abu82302	Novel	hum
285	36	81.8	1089	6	ABR62659	Abt662659	Human	sec		358	36	81.8	1089	6	ABU87313	Abu87313	Human	PRO
286	36	81.8	1089	6	ABR65659	Abt665659	Human	sec		359	36	81.8	1089	6	ABU83785	Abu83785	Human	sec
287	36	81.8	1089	6	ABU95599	Abu95599	Human	sec		360	36	81.8	1089	6	ABO08159	AbO08159	Human	PRO
288	36	81.8	1089	6	ABU82838	Abu82838	Human	PRO		361	36	81.8	1089	6	ABU81870	Abu81870	Novel	hum
289	36	81.8	1089	6	ABU89959	Abu89959	Novel	hum		362	36	81.8	1089	6	ABU66034	Abu66034	Novel	hum
290	36	81.8	1089	6	ABR68208	Abt68208	Human	sec		363	36	81.8	1089	6	ABR59863	Abt59863	Human	sec
291	36	81.8	1089	6	ABU96261	Abu96261	Novel	hum		364	36	81.8	1089	6	ABU94051	Abu94051	Novel	hum
292	36	81.8	1089	6	ABU92692	Abu92692	Human	sec		365	36	81.8	1089	6	ABU99904	Abu99904	Novel	hum
293	36	81.8	1089	6	ABO08769	AbO08769	Human	sec		366	36	81.8	1089	6	ABR66574	Abt66574	Human	sec
294	36	81.8	1089	6	ABO02821	AbO02821	Human	sec		367	36	81.8	1089	6	ABR90992	Abt90992	Human	sec
295	36	81.8	1089	6	ABR74975	Abt74975	Human	sec		368	36	81.8	1089	6	ABU94419	Abu94419	Human	PRO
296	36	81.8	1089	6	ABR94737	Abt94737	Human	sec		369	36	81.8	1089	6	ABU79301	Abu79301	Human	PRO
297	36	81.8	1089	6	ABU85710	Abu85710	Novel	hum		370	36	81.8	1089	6	ABU86630	Abu86630	Human	sec
298	36	81.8	1089	6	ABU98870	Abu98870	Novel	hum		371	36	81.8	1089	6	ABU86935	Abu86935	Novel	hum
299	36	81.8	1089	6	ABU98085	Abu98085	Novel	hum		372	36	81.8	1089	6	ABU94724	Abu94724	Human	PRO
300	36	81.8	1089	6	ABU91791	Abu91791	Novel	hum		373	36	81.8	1089	6	ABO04651	AbO04651	Human	PRO
301	36	81.8	1089	6	ABU89484	Abu89484	Human	PRO		374	36	81.8	1089	6	ABR70400	Abt70400	Human	sec
302	36	81.8	1089	6	ABU86325	Abu86325	Human	sec		375	36	81.8	1089	6	ABU98565	Abu98565	Human	PRO
303	36	81.8	1089	6	ABU67538	Abu67538	Human	sec		376	36	81.8	1089	6	ABR59855	Abt59855	Human	sec
304	36	81.8	1089	6	ABU80566	Abu80566	Human	PRO		377	36	81.8	1089	6	ABR64681	Abt64681	Human	sec
305	36	81.8	1089	6	ABR9484	Abt9484	Human	sec		378	36	81.8	1089	6	ABU79606	Abu79606	Human	PRO
306	36	81.8	1089	6	ABR98874	Abt98874	Human	sec		379	36	81.8	1089	6	ABU92997	Abu92997	Human	sec
307	36	81.8	1089	6	ABO16397	AbO16397	Human	sec		380	36	81.8	1089	6	ABU95956	Abu95956	Human	PRO
308	36	81.8	1089	6	ABR92297	Abt92297	Human	sec		381	36	81.8	1089	6	ABU91176	Abu91176	Novel	hum
309	36	81.8	1089	6	ABO18938	AbO18938	Human	sec		382	36	81.8	1089	6	ABO90269	AbO90269	Novel	hum
310	36	81.8	1089	6	ABR78359	Abt78359	Human	sec		383	36	81.8	1089	6	ABO09684	AbO09684	Human	sec
311	36	81.8	1089	6	ABU85095	Abu85095	Novel	hum		384	36	81.8	1089	6	ABO10956	AbO10956	Human	sec
312	36	81.8	1089	6	ABO00234	AbO00234	Novel	hum		385	36	81.8	1089	6	ABR71010	Abt71010	Human	sec
313	36	81.8	1089	6	ABO11566	AbO11566	Human	sec		386	36	81.8	1089	6	ABU87618	Abu87618	Human	PRO
314	36	81.8	1089	6	ABO02211	AbO02211	Human	sec		387	36	81.8	1089	6	ABU91486	Abu91486	Human	PRO
315	36	81.8	1089	6	ABU88785	Abu88785	Novel	hum		388	36	81.8	1089	6	ABU84700	Abu84700	Human	sec
316	36	81.8	1089	6	ABU83480	Abu83480	Human	sec		389	36	81.8	1089	6	ABR69790	Abt69790	Human	PRO
317	36	81.8	1089	6	ABO06281	AbO06281	Novel	hum		390	36	81.8	1089	6	ABU80167	Abu80167	Human	PRO

391	36	81.8	1089	6	ABU93436	Abu93436 Human PRO	464	36	81.8	1089	6	ABM08934	Abm08934 Human sec
392	36	81.8	1089	6	ABO09989	AbO09989 Human sec	465	36	81.8	1089	6	ABO36534	AbO36534 Human sec
393	36	81.8	1089	6	ABO09074	AbO09074 Human sec	466	36	81.8	1089	6	ABO35619	AbO35619 Human PRO
394	36	81.8	1089	6	ABU10642	AbU10642 Human sec	467	36	81.8	1089	6	ABO39584	AbO39584 Human sec
395	36	81.8	1089	6	ABU95651	AbU95651 Human PRO	468	36	81.8	1089	6	ABM10459	AbM10459 Human sec
396	36	81.8	1089	6	ABU96860	AbU96860 Novel hum	469	36	81.8	1089	6	ABM11984	AbM11984 Human sec
397	36	81.8	1089	6	ABR70705	AbR70705 Human sec	470	36	81.8	1089	6	ABO52130	AbO52130 Human PRO
398	36	81.8	1089	6	ABO05056	AbO05056 Novel hum	471	36	81.8	1089	6	ABO52435	AbO52435 Human PRO
399	36	81.8	1089	6	ABO08464	AbO08464 Human sec	472	36	81.8	1089	6	ABO23753	AbO23753 Human sec
400	36	81.8	1089	6	ABO05671	AbO05671 Human sec	473	36	81.8	1089	6	ABR97239	AbR97239 Human sec
401	36	81.8	1089	6	ABR74060	AbR74060 Human sec	474	36	81.8	1089	6	ABR87027	AbR87027 Human sec
402	36	81.8	1089	6	ABR95652	AbR95652 Human sec	475	36	81.8	1089	6	ABM11069	AbM11069 Human sec
403	36	81.8	1089	6	ABR80949	AbR80949 Human sec	476	36	81.8	1089	6	ABM28213	AbM28213 Human sec
404	36	81.8	1089	6	ABR81254	AbR81254 Human sec	477	36	81.8	1089	6	ABO32212	AbO32212 Human sec
405	36	81.8	1089	6	ABM00950	AbM00950 Human sec	478	36	81.8	1089	6	ABM15339	AbM15339 Human sec
406	36	81.8	1089	6	ABR88552	AbR88552 Human sec	479	36	81.8	1089	6	ABM06494	AbM06494 Human sec
407	36	81.8	1089	6	ABM77373	AbM77373 Human sec	480	36	81.8	1089	6	ABM04305	AbM04305 Human sec
408	36	81.8	1089	6	ABO28857	AbO28857 Human sec	481	36	81.8	1089	6	ABM22418	AbM22418 Human sec
409	36	81.8	1089	6	ABO31602	AbO31602 Human sec	482	36	81.8	1089	6	ABM07714	AbM07714 Human sec
410	36	81.8	1089	6	ABM08019	AbM08019 Human sec	483	36	81.8	1089	6	ABO40804	AbO40804 Human sec
411	36	81.8	1089	6	ABO40499	AbO40499 Human PRO	484	36	81.8	1089	6	ABM35451	AbM35451 Human sec
412	36	81.8	1089	6	ABO35924	AbO35924 Human PRO	485	36	81.8	1089	6	ABM33214	AbM33214 Human sec
413	36	81.8	1089	6	ABO44063	AbO44063 Human PRO	486	36	81.8	1089	6	ABO52740	AbO52740 Human PRO
414	36	81.8	1089	6	ADA78018	AdA78018 Human sec	487	36	81.8	1089	6	ABO50300	AbO50300 Human sec
415	36	81.8	1089	6	ABM24858	AbM24858 Human sec	488	36	81.8	1089	6	ABU99294	AbU99294 Human sec
416	36	81.8	1089	6	ABO03126	AbO03126 Human sec	489	36	81.8	1089	6	ABO04346	AbO04346 Human sec
417	36	81.8	1089	6	ABR90382	AbR90382 Human sec	490	36	81.8	1089	6	ABO05976	AbO05976 Human sec
418	36	81.8	1089	6	ABM17296	AbM17296 Human sec	491	36	81.8	1089	6	ABM18516	AbM18516 Human sec
419	36	81.8	1089	6	ABR95042	AbR95042 Human sec	492	36	81.8	1089	6	ABR97544	AbR97544 Human sec
420	36	81.8	1089	6	ABR95347	AbR95347 Human sec	493	36	81.8	1089	6	ABR80644	AbR80644 Human sec
421	36	81.8	1089	6	ABO21585	AbO21585 Human sec	494	36	81.8	1089	6	ABR81255	AbR81255 Human sec
422	36	81.8	1089	6	ABR97849	AbR97849 Human sec	495	36	81.8	1089	6	ABR88857	AbR88857 Human sec
423	36	81.8	1089	6	ABR87637	AbR87637 Human sec	496	36	81.8	1089	6	ABM13509	AbM13509 Human sec
424	36	81.8	1089	6	ABM77678	AbM77678 Human sec	497	36	81.8	1089	6	ABM20893	AbM20893 Human sec
425	36	81.8	1089	6	ABM27908	AbM27908 Human sec	498	36	81.8	1089	6	ABO42024	AbO42024 Human sec
426	36	81.8	1089	6	ABM06189	AbM06189 Human sec	499	36	81.8	1089	6	ABO42634	AbO42634 Human sec
427	36	81.8	1089	6	ABM03695	AbM03695 Human sec	500	36	81.8	1089	7	ADE50392	AdE50392 Human sec
428	36	81.8	1089	6	ABM35146	AbM35146 Human sec							
429	36	81.8	1089	6	ABM26383	AbM26383 Human sec							
430	36	81.8	1089	6	ABO48165	AbO48165 Human sec							
431	36	81.8	1089	6	ABR92907	AbR92907 Human sec							
432	36	81.8	1089	6	ABO24668	AbO24668 Human sec							
433	36	81.8	1089	6	ABM11679	AbM11679 Human sec							
434	36	81.8	1089	6	ABM02780	AbM02780 Human sec							
435	36	81.8	1089	6	ABM16076	AbM16076 Human sec							
436	36	81.8	1089	6	ABO27637	AbO27637 Human sec							
437	36	81.8	1089	6	ABM29128	AbM29128 Human sec							
438	36	81.8	1089	6	ABM07104	AbM07104 Human sec							
439	36	81.8	1089	6	ABM21198	AbM21198 Human sec							
440	36	81.8	1089	6	ABM09544	AbM09544 Human sec							
441	36	81.8	1089	6	ABO41414	AbO41414 Human sec							
442	36	81.8	1089	6	ABO36229	AbO36229 Human PRO							
443	36	81.8	1089	6	ABO43758	AbO43758 Human PRO							
444	36	81.8	1089	6	ABM76458	AbM76458 Human sec							
445	36	81.8	1089	6	ABM76154	AbM76154 Human sec							
446	36	81.8	1089	6	ABM25773	AbM25773 Human sec							
447	36	81.8	1089	6	ABM26078	AbM26078 Human sec							
448	36	81.8	1089	6	ABO03431	AbO03431 Human sec							
449	36	81.8	1089	6	ABO02516	AbO02516 Human sec							
450	36	81.8	1089	6	ABR90687	AbR90687 Human sec							
451	36	81.8	1089	6	ABR73785	AbR73785 Human sec							
452	36	81.8	1089	6	ABO17007	AbO17007 Human sec							
453	36	81.8	1089	6	ABR94432	AbR94432 Human sec							
454	36	81.8	1089	6	ABR75939	AbR75939 Human sec							
455	36	81.8	1089	6	ABR71315	AbR71315 Human sec							
456	36	81.8	1089	6	ABR93212	AbR93212 Human sec							
457	36	81.8	1089	6	ABR93517	AbR93517 Human sec							
458	36	81.8	1089	6	ABR87942	AbR87942 Human sec							
459	36	81.8	1089	6	ABO33611	Novel hum							
460	36	81.8	1089	6	ABO27942	Human sec							
461	36	81.8	1089	6	ABO30077	Human sec							
462	36	81.8	1089	6	ABO33286	Human PRO							
463	36	81.8	1089	6	ABM04974	AbM04974 Human sec							

464 36 81.8 1089 6 ABM08934 Abm08934 Human sec
465 36 81.8 1089 6 ABO36534 AbO36534 Human sec
466 36 81.8 1089 6 ABO35619 AbO35619 Human PRO
467 36 81.8 1089 6 ABO39584 AbO39584 Human sec
468 36 81.8 1089 6 ABM10459 AbM10459 Human sec
469 36 81.8 1089 6 ABM11984 AbM11984 Human sec
470 36 81.8 1089 6 ABO52130 AbO52130 Human PRO
471 36 81.8 1089 6 ABO52435 AbO52435 Human PRO
472 36 81.8 1089 6 ABO23753 AbO23753 Human sec
473 36 81.8 1089 6 ABR97239 AbR97239 Human sec
474 36 81.8 1089 6 ABR87027 AbR87027 Human sec
475 36 81.8 1089 6 ABM11069 AbM11069 Human sec
476 36 81.8 1089 6 ABM28213 AbM28213 Human sec
477 36 81.8 1089 6 ABO32212 AbO32212 Human sec
478 36 81.8 1089 6 ABM15339 AbM15339 Human sec
479 36 81.8 1089 6 ABM06494 AbM06494 Human sec
480 36 81.8 1089 6 ABM04305 AbM04305 Human sec
481 36 81.8 1089 6 ABM22418 AbM22418 Human sec
482 36 81.8 1089 6 ABM07714 AbM07714 Human sec
483 36 81.8 1089 6 ABO40804 AbO40804 Human sec
484 36 81.8 1089 6 ABM35451 AbM35451 Human sec
485 36 81.8 1089 6 ABM33214 AbM33214 Human sec
486 36 81.8 1089 6 ABO52740 AbO52740 Human PRO
487 36 81.8 1089 6 ABO50300 AbO50300 Human sec
488 36 81.8 1089 6 ABU99294 AbU99294 Human sec
489 36 81.8 1089 6 ABO04346 AbO04346 Human sec
490 36 81.8 1089 6 ABO05976 AbO05976 Human sec
491 36 81.8 1089 6 ABM18516 AbM18516 Human sec
492 36 81.8 1089 6 ABR97544 AbR97544 Human sec
493 36 81.8 1089 6 ABR80644 AbR80644 Human sec
494 36 81.8 1089 6 ABR81255 AbR81255 Human sec
495 36 81.8 1089 6 ABR88857 AbR88857 Human sec
496 36 81.8 1089 6 ABM13509 AbM13509 Human sec
497 36 81.8 1089 6 ABM20893 AbM20893 Human sec
498 36 81.8 1089 6 ABO42024 AbO42024 Human sec
499 36 81.8 1089 6 ABO42634 AbO42634 Human sec
500 36 81.8 1089 7 ADE50392 AdE50392 Human sec

ALIGNMENTS

RESULT 1
AAW95057
ID AAW95057 standard; peptide; 8 AA.
XX
AC AAW95057;
XX
DT 19-MAY-1999 (first entry)
XX
XX Anti-invasive and anti-angiogenic urokinase peptide fragment.
DE
XX Urokinase; anti-invasive; anti-angiogenic; variant; chemical derivative;
XX affinity ligand; pharmaceutical; inhibition; tumour invasion; metastasis;
KW peptidomimetic; cell migration; proliferation; angiogenesis; fibrosis;
KW atherosclerosis; post-Balloon angioplasty vascular restenosis; neointima;
KW vascular tumours; vascular graft restenosis; inflammatory; lung; scarring;
KW wound healing; psoriasis; venous thrombosis.
XX
XX Synthetic.
OS
XX
XX Key
FH Modified-site 1 Location/Qualifiers
FT /note= "N-terminal acetylation"
FT Modified-site 8 /note= "C-terminal amide"
FT
XX
XX W09905263-A1.
XX
XX
XX 04-FEB-1999.
XX
XX 24-JUL-1998; 98MO-US015437.
XX

PI Mazar AP, Jones TR;
 XX WPI, 2002-740743/80.
 XX
 PT Method for inhibiting invasiveness of tumor cells involves contacting the
 PT cells with a peptide compound or its derivative.
 PS
 XX Claim 1; Page 58; 87pp; English.
 CC The invention relates to inhibiting invasiveness of tumor cells and
 CC involves contacting the cells with a peptide compound (AB882273), its
 CC substitution variant, an addition variant having up to 10-15 additional
 CC amino acids, or a chemical derivative of the peptide or variant, or a
 CC peptidomimetic agent of the peptide. The peptide compound is useful for
 CC inhibiting cell migration, invasion, migration-induced cell proliferation
 CC or angiogenesis in a subject having a disease or condition (e.g. growth,
 CC invasion or metastasis of tumor such as brain tumor selected from
 CC astrocytoma, anaplastic astrocytoma, glioblastoma, glioblastoma
 CC multiforme, pilocytic astrocytoma, pleomorphic xanthoastrocytoma,
 CC subependymal giant cell astrocytoma, fibrillary astrocytoma, gemistocytic
 CC astrocytoma, protoplasmic astrocytoma, oligodendroglioma, anaplastic
 CC oligodendroglioma, ependymoma, anaplastic ependymoma, myxopapillary
 CC ependymoma, subependymoma, mixed oligoastrocytoma and malignant
 CC oligoastrocytoma or uterine disease such as endometriosis or pathogenic
 CC ocular neovascularization associated with or a cause of, proliferative
 CC diabetic retinopathy, neovascular age-related macular degeneration,
 CC retinopathy of prematurity, sickle cell retinopathy or retinal vein
 CC occlusion) associated with undesired cell migration, invasion, migration-
 CC induced proliferation, or angiogenesis and for inhibiting the
 CC invasiveness of tumor cells. Also for treating neovascular glaucoma,
 CC other retinopathy, retrolabial plaques and corneal diseases and in the
 CC treatment of fibrosis associated with a chronic inflammatory condition,
 CC lung fibrosis, chemotherapy-induced fibrosis, wound healing with scarring
 CC and fibrosis, psoriasis, atherosclerosis, myocardial angiogenesis, post-
 CC balloon angioplasty vascular restenosis, neointima formation following
 CC vascular trauma, vascular graft restenosis, coronary collateral
 CC formation, ischemic limb angiogenesis and deep venous thrombosis. The
 CC present sequence represents the peptide compound of the invention used for
 CC inhibiting tumor cell invasiveness
 CC
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 44; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSSPPEE 8
 Db 1 KPSSPPEE 8
 RESULT 4
 ADC66464
 ID ADC66464 standard; peptide; 8 AA.
 XX
 AC ADC66464;
 DT 18-DEC-2003 (first entry)
 XX
 DE Human urokinase plasminogen activator peptide (136-143).
 XX
 KW Human; urokinase plasminogen activator; uPA; cytosolic;
 KW antiatherosclerotic; vulnary; tranquillizer; antipsoriatic; vasotropic;
 KW thrombolytic; cell migration; cell invasion;
 KW migration-induced cell proliferation; angiogenesis;
 KW primary tumor growth; tumor invasion; metastasis; atherosclerosis;
 KW post-balloon angioplasty; vascular restenosis; neointima formation;
 KW vascular trauma; vascular graft restenosis; fibrosis;
 KW chronic inflammatory condition; lung fibrosis;
 KW chemotherapy-induced fibrosis; wound healing; scarring; psoriasis;
 KW deep venous thrombosis.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "Lys is optionally acetylated"
 FT Misc-difference 2
 FT /note= "This residue is optionally hydroxyproline"
 FT Misc-difference 5
 FT /note= "This residue is optionally hydroxyproline"
 FT Misc-difference 6
 FT /note= "This residue is optionally hydroxyproline"
 FT Modified-site 8
 FT /note= "Glu is optionally amidated "
 XX
 PN US2003027768-A1.
 XX
 PD 06-FEB-2003.
 XX
 PF 06-SEP-2002; 2002US-00235552.
 XX
 PR 25-JUL-1997; 97US-00900327.
 PR 10-NOV-1999; 99US-00437136.
 XX
 PA (MAZA/) MAZAR A P.
 PA (JONE/) JONES T R.
 PI Mazar AP, Jones TR;
 XX WPI, 2003-765298/72.
 DR
 XX Novel peptide or its variants for inhibiting the invasiveness of tumor
 PT cells, for treating disease or condition such as primary tumor growth,
 PT atherosclerosis, or fibrosis associated with chronic inflammatory
 PT condition.
 XX
 PS Claim 1; SEQ ID NO 2; 52pp; English.
 XX
 CC The invention relates to a peptide compound appearing as ADC66464, or its
 CC substitution variant, addition variant or other chemical derivative. The
 CC peptide represents amino acids 136-143 of Human urokinase plasminogen
 CC activator, uPA. Also included are multimer of ADC66464 or its variants
 CC and a pharmaceutical composition (PC) useful for inhibiting invasion of
 CC tumor cells or angiogenesis, comprising ADC66464 and a carrier or
 CC excipient. The uPA peptide is useful for inhibiting the invasiveness of
 CC tumor cells. (PC) is useful for inhibiting cell migration, invasion,
 CC migration-induced cell proliferation or angiogenesis in a subject having
 CC a disease or condition associated with undesired cell migration,
 CC invasion, migration-induced proliferation, or angiogenesis. The disease
 CC or condition is primary tumor growth, tumor invasion or metastasis,
 CC atherosclerosis, post-balloon angioplasty, vascular restenosis, neointima
 CC formation following vascular trauma, vascular graft restenosis, fibrosis
 CC associated with a chronic inflammatory condition, lung fibrosis,
 CC chemotherapy-induced fibrosis, wound healing with scarring and fibrosis,
 CC psoriasis, deep venous thrombosis, or another disease or condition in
 CC which angiogenesis is pathogenic. The present sequence is the uPA peptide
 CC of the invention.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 44; DB 7; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSSPPEE 8
 Db 1 KPSSPPEE 8
 RESULT 5
 AAM95058
 ID AAM95058 standard; peptide; 9 AA.
 XX
 AC AAM95058;
 XX

DT 19-MAY-1999 (first entry)
 XX Urokinase peptide fragment A14.
 DE
 XX
 XX Urokinase; anti-invasive; anti-angiogenic; variant; chemical derivative;
 KM affinity ligand; pharmaceutical; inhibition; tumour invasion; metastasis;
 KM peptidomimetic; cell migration; proliferation; angiogenesis; fibrosis;
 KM atherosclerosis; post-balloon angioplasty vascular restenosis; neointima;
 KM vascular trauma; vascular graft restenosis; inflammatory; lung; scarring;
 KM wound healing; psoriasis; venous thrombosis.
 XX
 XX Synthetic.
 OS
 XX WO9905263-A1.
 PN
 XX 04-FEB-1999.
 PD
 XX 24-JUL-1998; 98WO-US015437.
 PF
 XX 25-JUL-1997; 97US-00900327.
 PR
 XX (ANGS-) ANGSTROM PHARM INC.
 PA
 XX Jones TR, Mazar AP;
 PI
 XX MPI; 1999-142921/12.
 DR
 XX
 XX New urokinase peptides and derivatives with anti-invasive and anti-
 PT angiogenic activity - useful for treating diseases or conditions
 PT associated with undesired cell migration, invasion, migration-induced
 PT proliferation, or angiogenesis.
 XX
 XX Example 2; Page 44; 73pp; English.
 PS
 XX The invention relates to an anti-invasive and anti-angiogenic peptide
 CC compound. The compound has a sequence corresponding to that shown in
 CC AA95057 or a substitution variant, addition variant or other chemical
 CC derivative of that peptide. The peptide or its variant or a derivative
 CC can be capped or uncapped. The peptides are useful for in vivo or in
 CC vitro prognostic and diagnostic applications, e.g. as labelled peptides
 CC of a cell (see AA95057 for detailed uses of the peptide compound, its
 CC variants/derivatives). The present sequence represents a urokinase
 CC peptide fragment tested along with the peptide of the invention for anti-
 CC invasive activity
 CC
 XX Sequence 9 AA;
 SQ
 Query Match 100.0%; Score 44; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSSPPEE 8
 DB 1 KPSSPPEE 8
 ID AA95056 standard; peptide; 10 AA.
 XX
 XX AA95056;
 AC
 XX 19-MAY-1999 (first entry)
 DT
 XX Urokinase peptide fragment.
 DE
 XX Urokinase; anti-invasive; anti-angiogenic; variant; chemical derivative;
 KM affinity ligand; pharmaceutical; inhibition; tumour invasion; metastasis;
 KM peptidomimetic; cell migration; proliferation; angiogenesis; fibrosis;
 KM atherosclerosis; post-balloon angioplasty vascular restenosis; neointima;
 KM vascular trauma; vascular graft restenosis; inflammatory; lung; scarring;
 KM wound healing; psoriasis; venous thrombosis.
 XX

XX Synthetic.
 OS
 XX WO9905263-A1.
 PN
 XX 04-FEB-1999.
 PD
 XX 24-JUL-1998; 98WO-US015437.
 PF
 XX 25-JUL-1997; 97US-00900327.
 PR
 XX (ANGS-) ANGSTROM PHARM INC.
 PA
 XX Jones TR, Mazar AP;
 PI
 XX MPI; 1999-142921/12.
 DR
 XX
 XX New urokinase peptides and derivatives with anti-invasive and anti-
 PT angiogenic activity - useful for treating diseases or conditions
 PT associated with undesired cell migration, invasion, migration-induced
 PT proliferation, or angiogenesis.
 XX
 XX Example 2; Page 43; 73pp; English.
 PS
 XX The invention relates to an anti-invasive and anti-angiogenic peptide
 CC compound. The compound has a sequence corresponding to that shown in
 CC AA95057 or a substitution variant, addition variant or other chemical
 CC derivative of that peptide. The peptide or its variant or a derivative
 CC can be capped or uncapped. The peptides are useful for in vivo or in
 CC vitro prognostic and diagnostic applications, e.g. as labelled peptides
 CC of a cell (see AA95057 for detailed uses of the peptide compound, its
 CC variants/derivatives). The present sequence represents a urokinase
 CC peptide fragment tested along with the peptide of the invention for anti-
 CC invasive activity
 CC
 XX Sequence 10 AA;
 SQ
 Query Match 100.0%; Score 44; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSSPPEE 8
 DB 1 KPSSPPEE 8
 ID ABB82272 standard; peptide; 10 AA.
 XX
 XX ABB82272;
 AC
 XX 08-JAN-2003 (first entry)
 DT
 XX Plasminogen activator uPA tryptic phosphopeptide (residues 136-145).
 DE
 XX Plasminogen; uPA; tumour; cytostatic; ophthalmological; antidiabetic;
 KM antiproliferative; anti-inflammatory; vasodilator; gynaecological;
 KM antiarteriosclerotic; thrombolytic.
 KM
 XX Unidentified.
 OS
 XX WO200269885-A2.
 PN
 XX 12-SEP-2002.
 PD
 XX 22-JAN-2002; 2002WO-US001560.
 PF
 XX 19-JAN-2001; 2001US-0262422P.
 PR
 XX (ANGS-) ANGSTROM PHARM INC.
 PA
 XX

FT Region 1..7
 FT /note= "t-PA residues 955-975"
 FT 8..21
 FT /note= "u-PA-II residues 134-147"
 XX
 XX WO8608451-A.
 XX
 PD 03-NOV-1988.
 XX
 XX 28-APR-1988; 88WO-NL000020.
 XX
 XX 29-APR-1987; 87NL-00001021.
 XX
 PA (BLOE-) STICHT LAB BLOEDTRA.
 PA (NERO-) NEDERLAND RODE KRUI.
 XX
 PI Pannekoek H;
 DR WPI; 1988-322771/45.
 DR N-PSDB; AAN81682.
 XX
 PT Mutant plasminogen activator protein(s) - contg. a t-PA portion including
 PT the H chain and a u-PA portion including the B chain.
 XX
 PS Disclosure; Fig 1; 39pp; English.
 XX
 CC t-PA/u-PA substitution-mutant proteins t-PA::u-PA-I and t-PA::U-PA-II are
 CC claimed. The mutant is much more effective in plasminogen activation in
 CC the presence of fibrin and is more resistant to inactivation by a PA
 CC inhibitor. It is used in pharmaceutical compsn. having an effect on blood
 CC clotting and/or on fibrinolysis. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 44; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
 DB 10 KPSSPPEE 17

RESULT 10

AAW22737
ID AAW22737 standard; peptide; 21 AA.

AC AAW22737;

DT 12-MAR-1998 (first entry)

DE Linking sequence from metastasis inhibitor.

KW Chimeric; human; urinary trypsin; inhibitor; HI-8; cancer; metastasis;
 KW G-domain; urokinase; prevention; leukaemia; lymphoma.

OS Synthetic.

PN WO9725422-A1.

PD 17-JUL-1997.

PF 06-JAN-1997; 97WO-JP000008.

PR 08-JAN-1996; 96JP-00001059.

PA (NISP) NISSIN FOOD PROD CO LTD.

PI Kobayashi H, Terao T, Sugino D, Okushima M;

DR WPI; 1997-372862/34.

PT Chimeric protein which inhibits development of metastases in cancer -
 PT contains urinary trypsin inhibitor carboxy-terminal domain linked to
 PT urokinase G-domain.
 XX
 XX Claim 2; Page 68; 97pp; Japanese.
 PS
 CC A novel chimeric protein contains the carboxy-terminal domain of human
 CC urinary trypsin inhibitor (HI-8), which inhibits cancer cell metastasis,
 CC linked to a peptide containing the G-domain of urokinase (AAW22742),
 CC which specifically binds the excess urokinase receptor expressed in
 CC cancer cells. The chimeric protein has the amino-terminal AAW22734, the
 CC carboxy-terminal AAW22735 and a linking sequence selected from AAW22736-
 CC 39 or partial sequences derived from these, specifically AAW8130-63. The
 CC chimeric protein may also have additional amino-terminal sequences
 CC selected from AAW22740 or 9 partial sequences derived from this, and/or
 CC additional carboxy-terminal sequences selected from AAW22743 or 10
 CC partial sequences derived from this. The chimeric protein can be used to
 CC prevent metastasis in, e.g. cancer of the lung, kidney, pancreas,
 CC stomach, colon, rectum, ovary, uterus, brain, skin, muscle, breast or
 CC prostate, and in leukaemia or lymphoma
 XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 44; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
 DB 5 KPSSPPEE 12

RESULT 11

AAE16550
ID AAE16550 standard; protein; 96 AA.

AC AAE16550;

DT 09-APR-2002 (first entry)

DE Human uPA kringle and connecting peptide.

KW Human; urokinase-type plasminogen activator; uPA; therapy; hypertension;
 KW stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder;
 KW microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma;
 KW tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing;
 KW clotting disorder; uterine contraction disorder; respiratory disease;
 KW adult respiratory distress syndrome; male impotence.
 XX
 OS Homo sapiens.

PN WO200197752-A2.

PD 27-DEC-2001.

PF 13-JUN-2001; 2001WO-US018976.

PR 20-JUN-2000; 2000US-0212874P.

PA (UYPR-) UNIV PENNSYLVANIA.

PI Cines DB, Higazi AA;

DR WPI; 2002-122240/16.

DR N-PSDB; AAD27083.

PT Composition for modulating muscle cell and tissue contractility for
 PT treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
 PT comprising domains from urokinase-type plasminogen activator.
 XX
 PS Claim 25; Fig 11; 117pp; English.

The invention relates to a composition comprising one or more domains of

CC urokinase-type plasminogen activator (uPA). The composition is used to
 CC modulate the contractility and angiogenic activity of a mammalian muscle,
 CC endothelial cell or tissue. The composition is used for treating stroke,
 CC hypertension, atherosclerosis, heart attack, microvascular
 CC occlusions, thrombotic microangiopathies, surgically induced thrombotic
 CC disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
 CC invasion, tumour cell angiogenesis, tumour cell metastasis, glioma,
 CC diabetic retinopathy, wound healing, clotting disorder, uterine
 CC contraction disorder, male impotence, respiratory disease or condition
 CC such as asthma, adult respiratory distress syndrome, primary pulmonary
 CC hypertension, microvascular thrombotic occlusion, and a disorder
 CC associated with chronic intrapulmonary fibrin formation. The present
 CC sequence is human urokinase-type plasminogen activator (uPA) kringles and
 CC connecting peptide

CC Sequence 96 AA;

Query Match 100.0%; Score 44; DB 5; Length 96;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSSPPEE 8
 DB 89 KPSSPPEE 96

RESULT 12
 AAE16549
 ID AAE16549 standard; protein; 143 AA.
 AC AAE16549;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human uPA amino terminal fragment (ATF) and connecting peptide.
 XX
 XX Human; urokinase-type plasminogen activator; uPA; therapy; hypertension;
 XX stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder;
 XX microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma;
 XX tumour cell metastasis; glioma; diabetic retinopathy; wound healing;
 XX clotting disorder; uterine contraction disorder; respiratory disease;
 XX adult respiratory distress syndrome; amino terminal fragment; ATF;
 XX male impotence.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO200197752-A2.
 PN
 XX
 PD 27-DEC-2001.
 XX
 XX 13-JUN-2001; 2001WO-US018976.
 PF
 XX
 XX 20-JUN-2000; 2000US-0212874P.
 PR
 XX
 XX (UYPE-) UNIV PENNSYLVANIA.
 PA
 XX
 XX Cines DB, Higazi AA;
 PI
 XX
 XX WPI; 2002-122240/16.
 DR
 XX
 XX N-PSDB; AAD27082.
 DR
 XX
 XX Composition for modulating muscle cell and tissue contractility for
 PT treating atherosclerosis, asthma, hypertension, glioma, impotence,
 PT comprising domains from urokinase-type plasminogen activator.
 PT
 XX
 XX Claim 24; Fig 1H; 117pp; English.
 PS
 XX
 XX The invention relates to a composition comprising one or more domains of
 CC urokinase-type plasminogen activator (uPA). The composition is used to
 CC modulate the contractility and angiogenic activity of a mammalian muscle,
 CC endothelial cell or tissue. The composition is used for treating stroke,
 CC hypertension, atherosclerosis, heart attack, microvascular
 CC occlusions, thrombotic microangiopathies, surgically induced thrombotic
 CC disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
 CC invasion, tumour cell angiogenesis, tumour cell metastasis, glioma,
 CC diabetic retinopathy, wound healing, clotting disorder, uterine
 CC contraction disorder, male impotence, respiratory disease or condition
 CC such as asthma, adult respiratory distress syndrome, primary pulmonary
 CC hypertension, microvascular thrombotic occlusion, and a disorder
 CC associated with chronic intrapulmonary fibrin formation. The present
 CC sequence is human urokinase-type plasminogen activator (uPA) amino
 CC terminal fragment (ATF) and connecting peptide

CC disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
 CC invasion, tumour cell angiogenesis, tumour cell metastasis, glioma,
 CC diabetic retinopathy, wound healing, clotting disorder, uterine
 CC contraction disorder, male impotence, respiratory disease or condition
 CC such as asthma, adult respiratory distress syndrome, primary pulmonary
 CC hypertension, microvascular thrombotic occlusion, and a disorder
 CC associated with chronic intrapulmonary fibrin formation. The present
 CC sequence is human urokinase-type plasminogen activator (uPA) amino
 CC terminal fragment (ATF) and connecting peptide

CC Sequence 143 AA;

Query Match 100.0%; Score 44; DB 5; Length 143;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSSPPEE 8
 DB 136 KPSSPPEE 143

RESULT 13
 AAM22747
 ID AAM22747 standard; protein; 208 AA.
 XX
 XX AAM22747;
 AC
 XX
 DT 12-MAR-1998 (first entry)
 XX
 DE Metastasis inhibitor.
 XX
 XX Chimeric; human; urinary trypsin; inhibitor; HI-8; cancer; metastasis;
 XX G-domain; urokinase; prevention; leukaemia; lymphoma.
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO9725422-A1.
 PN
 XX
 PD 17-JUL-1997.
 XX
 XX 06-JAN-1997; 97MO-JP000008.
 PF
 XX
 XX 08-JAN-1996; 96JP-00001059.
 PR
 XX
 XX (NISP) NISSIN FOOD PROD CO LTD.
 PA
 XX
 XX Kobayashi H, Terao T, Sugino D, Okushima M;
 PI
 XX
 XX WPI; 1997-372862/34.
 DR
 XX
 XX N-PSDB; AAT75155.
 DR
 XX
 XX Chimeric protein which inhibits development of metastases in cancer -
 PT Best local similarity which inhibits development of metastases in cancer -
 PT urokinase G-domain.
 PT
 XX
 XX Claim 19; Page 59-60; 97pp; Japanese.
 PS
 XX
 XX The present sequence is a novel chimeric protein, which contains the
 CC carboxy-terminal domain of human urinary trypsin inhibitor (HI-8), which
 CC inhibits cancer cell metastasis; linked to a peptide containing the G-
 CC domain of urokinase, which specifically binds the excess urokinase
 CC receptor expressed in cancer cells. The chimeric protein can be used to
 CC prevent metastasis in, e.g. cancer of the lung, kidney, pancreas,
 CC stomach, colon, rectum, ovary, uterus, brain, skin, muscle, breast or
 CC prostate, and in leukaemia or lymphoma
 CC
 XX
 XX Sequence 208 AA;

Query Match 100.0%; Score 44; DB 2; Length 208;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSSPPEE 8

```

Db          |||||
           137 KPSSPPE 144

RESULT 14
AA63140
ID  AA63140 standard; protein; 259 AA.
XX
XX
AC  AA63140;
XX
XX  25-MAR-2003 (revised)
DT  02-JUN-1995 (first entry)
XX
XX  Low molecular weight urokinase bioactive protein.
DE
XX  Urokinase bioactive glycoprotein; cardiovascular diseases;
KM  pulmonary embolism.
XX
XX  Homo sapiens.
OS
XX  EP620279-A1.
PN
XX  19-OCT-1994.
PD
XX  14-APR-1983; 94EP-00104777.
PF
XX  15-APR-1982; 82US-00368773.
PR  14-MAR-1983; 83US-00474930.
PR  14-APR-1983; 83EP-00103629.
XX
XX  (GETH ) GENENTECH INC.
PA
XX
XX  Heyneker HL, Holmes WE, Vehar GA;
PI
XX  WPI; 1994-318362/40.
DR
XX  N-PSDB; AAQ73481.
DR
XX
XX  Prodn. of human urokinase glycoprotein - using a recombinant expression
PT  system used for the treatment of vascular diseases or conditions.
PT
XX
XX  Claim 6; Fig 2; 41pp; English.
PS
XX
XX  AAQ73481 is the cDNA sequence which encodes AA63140 a low molecular
CC  weight 33000 dalton urokinase (UK) bioactive protein. This cDNA was used
CC  in the construction of a plasmid capable of transforming either yeast or
CC  vertebrate cells, enabling them to produce the 33000 dalton UK bioactive
CC  protein. The UK glycoprotein produced could then be used in the treatment
CC  of cardiovascular diseases, including pulmonary embolism. The UK produced
CC  using this method had the advantage of a specific activity towards fibrin
CC  and extant thrombi, not demonstrated previously with UK isolated from
CC  natural sources. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC  on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC  PR field.)
XX
XX  Sequence 259 AA;
SQ

Query Match          100.0%; Score 44; DB 2; Length 259;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 KPSSPPE 8
   |||||
Db  4 KPSSPPE 11

RESULT 15
AA61546
ID  AA61546 standard; protein; 276 AA.
XX
XX
AC  AA61546;
XX
XX  09-APR-2002 (first entry)
XX

```

```

DE  Human LMW-urokinase-type plasminogen activator (uPA) protein.
XX
XX  Human; urokinase-type plasminogen activator; uPA; therapy; hypertension;
KM  stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder;
KM  microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma;
KM  tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing;
KM  clotting disorder; uterine contraction disorder; respiratory disease;
KM  male impotence; adult respiratory distress syndrome; LMW-uPA.
XX
XX  Homo sapiens.
OS
XX  WO200197752-A2.
PN
XX
XX  27-DEC-2001.
PD
XX
XX  13-JUN-2001; 2001MO-US018976.
PF
XX  20-JUN-2000; 2000US-0212874P.
PR
XX  (UYPE-) UNIV PENNSYLVANIA.
PA
XX  Cines DB, Higazi AA;
PI
XX
XX  WPI; 2002-122240/16.
DR  N-PSDB; AAD27079.
DR
XX
XX  Composition for modulating muscle cell and tissue contractility for
PT  treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
PT  comprising domains from urokinase-type plasminogen activator.
XX
XX  Claim 5; Fig 1E; 117pp; English.
PS
XX
XX  The invention relates to a composition comprising one or more domains of
CC  urokinase-type plasminogen activator (uPA). The composition is used to
CC  modulate the contractility and angiogenic activity of a mammalian muscle,
CC  endothelial cell or tissue. The composition is used for treating stroke,
CC  hypotension, hypertension, atherosclerosis, heart attack, microvascular
CC  occlusions, thrombotic microangiopathies, surgically induced thrombotic
CC  disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
CC  invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma,
CC  diabetic retinopathy, wound healing, clotting disorder, uterine
CC  contraction disorder, male impotence, respiratory disease or condition
CC  such as asthma, adult respiratory distress syndrome, primary pulmonary
CC  hypertension, microvascular thrombotic occlusion, and a disorder
CC  associated with chronic intrapulmonary fibrin formation. The present
CC  sequence is human LMW-urokinase-type plasminogen activator (uPA) protein
XX
XX  Sequence 276 AA;
SQ

Query Match          100.0%; Score 44; DB 5; Length 276;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 KPSSPPE 8
   |||||
Db  1 KPSSPPE 8

RESULT 16
AA61548
ID  AA61548 standard; protein; 323 AA.
XX
XX
AC  AA61548;
XX
XX  09-APR-2002 (first entry)
XX
XX  Human uPA deltkringle-secuPA and deltkringle-tcuPA mutant.
DE
XX
XX  Human; urokinase-type plasminogen activator; uPA; therapy; hypertension;
KM  stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder;
KM  microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma;
KM  tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing;
KM  clotting disorder; uterine contraction disorder; respiratory disease;

```

XX	male impotence; adult respiratory distress syndrome; tcupA; scuPA;
KW	two chain urokinase; single chain urokinase; mutant; mutein.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	MO20019752-A2.
XX	
XX	27-DEC-2001.
XX	
PF	13-JUN-2001; 2001WO-US018976.
XX	
XX	20-JUN-2000; 2000US-0212874P.
PR	
PA	(TYPE-) UNIV PENNSYLVANIA.
XX	
PI	Clines DB, Higazi AA;
XX	
DR	WPI; 2002-122240/16.
DR	N-PSDB; AAD27081.
XX	
PT	Composition for modulating muscle cell and tissue contractility for
PT	treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
PT	comprising domains from urokinase-type plasminogen activator.
XX	
PS	Claim 23; Fig 1G; 117pp; English.
XX	
CC	The invention relates to a composition comprising one or more domains of
CC	urokinase-type plasminogen activator (uPA). The composition is used to
CC	modulate the contractility and angiogenic activity of a mammalian muscle,
CC	endothelial cell or tissue. The composition is used for treating stroke,
CC	hypertension, hypertension, atherosclerosis, heart attack, microvascular
CC	occlusions, thrombotic microangiopathies, surgically induced thrombotic
CC	disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
CC	invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma,
CC	diabetic retinopathy, wound healing, clotting disorder, uterine
CC	contraction disorder, male impotence, respiratory disease or condition
CC	such as asthma, adult respiratory distress syndrome, primary pulmonary
CC	hypertension, microvascular thrombotic occlusion, and a disorder
CC	associated with chronic interpulmonary fibrin formation. The present
CC	sequence is human urokinase-type plasminogen activator (uPA) deltatrangle
CC	single chain urokinase (scuPA) and deltatrangle-two chain urokinase
CC	(tcuPA) deletion mutant
XX	
SQ	Sequence 323 AA;
XX	
Query Match	100.0%; Score 44; DB 5; Length 323;
Best Local Similarity	100.0%; Pred. No. 82;
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 KPSSPPEE 8
DB	48 KPSSPPEE 55
XX	
RESULT 17	
ID	AAG75492 standard; protein; 337 AA.
XX	AAG75492;
AC	AAG75492;
XX	
DT	03-SEP-2001 (first entry)
XX	
DE	Human colon cancer antigen protein SEQ ID NO:6256.
XX	
KW	Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW	colorectal carcinoma; chromosome 10.
XX	
OS	Homo sapiens.
OS	
PN	MO200122920-A2.
XX	
DB	05-APR-2001.

PF		28-SEP-2000; 2000MO-USO26524.				
XX						
XX		29-SEP-1999; 99US-0157137P.				
PR		03-NOV-1999; 99US-0163280P.				
XX						
PA	(HUMA-) HUMAN GENOME SCI INC.					
XX						
P1	Ruben SM, Barash SC, Birse CE, Rosen CA;					
DR	WP1; 2001-235357/24.					
DR	N-PSDB; AAH34897.					
PT	Nucleic acids encoding 4277 human colon cancer-associated polypeptides,					
PI	useful for preventing, diagnosing and/or treating colorectal cancers.					
XX						
PS	Claim 11; Page 7707-7708; 9803pp; English.					
CC						
CC	AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon					
CC	cancer-associated nucleic acid molecules (N) and proteins (P), where the					
CC	proteins are collectively known as colon cancer antigens. The colon					
CC	cancer antigens have cytoprotective activity and can be used in gene therapy					
CC	and vaccine production. N and P may be used in the prevention, diagnosis					
CC	and treatment of diseases associated with inappropriate P expression. For					
CC	example, N and P may be used to treat disorders associated with decreased					
CC	expression by rectifying mutations or deletions in a patient's genome					
CC	that affect the activity of P by expressing inactive proteins or to					
CC	supplement the patients own production of P. Additionally, N may be used					
CC	to produce the colon cancer-associated Ps, by inserting the nucleic acids					
CC	into a host cell and culturing the cell to express the proteins. N and P					
CC	can be used in the prevention, diagnosis and treatment of colorectal					
CC	carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent					
CC	sequences used in the exemplification of the present invention. N.B.					
CC	Pages 666 to 682 and page 7053 of the sequence listing were missing at					
CC	time of publication, meaning no sequences are present for SEQ ID NO:1027					
CC	to 1052, 7921 and 7922					
SQ						
SQ	Sequence 337 AA;					
	Query Match	100.0%; Score 44; DB 4; Length 337;				
	Best Local Similarity	100.0%; Prod. No. 85;				
	Matches	8; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
OY		1 KPSSPPER	8			
DB		162 KPSSPPER	169			
	RESULT 18					
	ABP41795					
ID	ABP41795 standard; protein, 337 AA.					
XX						
AC	ABP41795;					
XX						
DFT						
DE	22-AUG-2002 (first entry)					
XX						
XX	Human ovarian antigen HVVCB79, SEQ ID NO:2927.					
KW	Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;					
KM	infectious cancer; breast cancer; tumour; reproductive system disorder;					
KM	fertility; pregnancy disorder; anovulation; polycystic ovary syndrome;					
KM	PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;					
KM	inflammatory condition; immune disorder; blood disorder;					
KM	cardiovascular disorder; respiratory disorder; neurological disorder;					
KM	gastrointestinal disorder; urinary system disorder; drug screening;					
KM	gene therapy; chromosome mapping; forensic analysis;					
KM	antibody preparation; cytostatic; immunomodulatory; neuroprotective;					
XX	antiinflammatory; gynaecological; reproductive; chromosome 10q24.					
OS	Homo sapiens.					
FN	WO200200677-A1.					
XX						

PD 03-JAN-2002.
 XX 07-JUN-2001; 2001WO-US018569.
 PF 07-JUN-2000; 2000US-0209467P.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Blire CE, Rosen CA;
 PI WPI; 2002-147878/19.
 XX N-PSDB; ABQ54872.
 DR
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX
 XX Claim 11; SEQ ID NO 2927; 2922pp; English.
 XX
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovarian and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumors of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 337 AA;
 SO

Query Match 100.0%; Score 44; DB 5; Length 337;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
 DB 162 KPSSPPEE 169

RESULT 19
 AAR68854
 ID AAR68854 standard; protein; 365 AA.
 XX
 AC AAR68854;
 XX
 XX 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 22-NOV-1995 (first entry)
 XX
 XX Delta 1-46 urokinase.
 DE
 XX

KW Human; des-epidermal growth factor homologous plasminogen activator; uPA;
 KW liver membrane; reduced affinity; EGF homologous; thrombosis;
 KW thrombolytic; increased half-life; urokinase.
 XX
 XX Homo sapiens; (engineered).
 OS
 XX Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "amino acids 1-46 of wild-type urokinase have been
 FT deleted"
 XX
 XX US5376547-A.
 XX
 XX 27-DEC-1994.
 PD
 XX 29-JUN-1988; 88US-00150267.
 PF
 XX 30-JAN-1987; 87US-00008795.
 PR
 XX (AMHP) AMERICAN HOME PROD CORP.
 PA
 XX Hung PP, Lee SL, Kalyan NK;
 PI WPI; 1995-043464/06.
 DR
 XX
 XX New modified plasminogen activator cpds. - having regions removed to
 PT reduce affinity for liver membranes and increase circulation half-life.
 PT
 XX Claim 1; Page 7; 26pp; English.
 PS
 XX Amino acid residues 1-46 contain the EGF region of human urokinase.
 CC Deletion of this region results in a plasminogen activator with reduced
 CC affinity for liver cell membranes; the mutant protein is not cleared from
 CC the circulation as rapidly as is wild-type tPA. The specification only
 CC gives the sequence around the deletion and not the full-length sequence
 CC of "delta 1-46 urokinase"; the sequence in AAR68854 has been obtained by
 CC amending a previously disclosed wild-type human urokinase sequence (from
 CC W09501427) according to the description given in Example 3. (Updated on
 CC 25-MAR-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise
 CC OS field)
 CC
 XX Sequence 365 AA;
 SO

Query Match 100.0%; Score 44; DB 2; Length 365;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
 DB 90 KPSSPPEE 97

RESULT 20
 AAM13635
 ID AAM13635 standard; protein; 378 AA.
 XX
 AC AAM13635;
 XX
 XX 04-JUN-1997 (first entry)
 DT
 XX Human prourokinase variant lacking entire EGF domain.
 DE
 XX Human; prourokinase; hPUK; variant; half-life; increase; EGF;
 KW epidermal growth factor domain; deletion; thrombolysis; fibrinolysis.
 KW
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX Key Location/Qualifiers
 FT 1.
 FT /note= "residues 1-9 of native hPUK"
 FT 10..378
 FT /note= "residues 43-411 of native hPUK"
 FT

FT	Misc-difference 144	/note= "corresponds to TAC codon"
XX		
PN	EP398361-A.	
PD	22-NOV-1990.	
PF	18-MAY-1990;	90EP-00109472.
PR	18-MAY-1989;	89JP-00126433.
PR	22-FEB-1990;	90JP-00042020.
PA	(GREEN) GREEN CROSS CORP.	
PI	Tanabe T, Amatsuji Y, Kasai S, Hirose M, Morita M, Kawabe H;	
PI	Airmura H;	
XX		
DR	WPI; 1990-350146/47.	
DR	N-PSDB; AAT61672.	
PT	Human pro-urokinase variants - deficient in loop regions of epidermal growth factor, showing long blood half-life, as fibrinolytic agent.	
XX		
PS	Claim 1; Page; 22pp; English.	
XX		
CC	New variants of human prourokinase (hPUK) comprise a hPUK deficient in	
CC	(1) at least part of the first loop region of the epidermal growth factor	
CC	(EGF) domain; (ii) at least part of the first loop and at least part of	
CC	the second loop; or (iii) at least part of the third loop. The hPUK	
CC	variants show an increased blood half-life comparable to that of the	
CC	whole EGF domain-deficient hPUK variant and urokinase while retaining the	
CC	same properties as those of hPUK. They have potent thrombolytic activity	
CC	and very little tendency to cause spontaneous bleeding. The present	
CC	sequence represents a specific variant of hPUK which lacks the entire EGF	
CC	domain; the sequence does not appear in the specification and has been	
CC	created using the wild-type hPUK sequence and the junction sequence after	
CC	deletion, both of which are given (in Fig 1 and in Fig 2(3)),	
CC	respectively)	
XX		
SQ	Sequence 378 AA;	
	Query Match 100.0%; Score 44; DB 2; Length 378;	
	Best Local Similarity 100.0%; Pred. No. 95;	
	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
OY	1 KPSSPPEE 8	
Db	103 KPSSPPEE 110	
RESULT 21		
AAR66266		
ID	AAR66266 standard; protein; 386 AA.	
XX		
AC	AAR66266;	
XX		
DT	25-MAR-2003 (revised)	
DT	17-AUG-1995 (first entry)	
XX		
DE	Bifunctional urokinase variant M33.	
XX		
KW	fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;	
KW	urokinase; variant; mutein.	
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
FT	Region	1..365
FT		/label= M4
FT		/note= "unglycosylated prourokinase(Ser47-Leu411)"
FT	Disulfide-bond	4..85
FT	Disulfide-bond	25..67
FT	Disulfide-bond	56..80

FT	Disulfide-bond	102.	.233	
FT	Disulfide-bond	143.	.159	
FT	Disulfide-bond	151.	.222	
FT	Disulfide-bond	247.	.316	
FT	Disulfide-bond	279.	.295	
FT	Disulfide-bond	306.	.334	
FT	Disulfide-bond	365.	.366	
FT	Region	/label= X1		
FT	Region	/note= "peptide bond"		
FT	Region	366.	.386	
FT	Region	/label= Y1		
XX				
XX	DE4323754-C1.			
XX				
XX	01-DEC-1994.			
XX				
XX	15-JUL-1993;	93DE-04323754.		
XX				
XX	15-JUL-1993;	93DE-04323754.		
XX				
PA	(CHEF) GRUENENTHAL GMBH.			
XX				
PI	Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;			
PI	Saunders DJ;			
XX				
DR	WPI, 1995-015191/03.			
XX				
PT	New bifunctional urokinase derive and related plasmids - with improved			
PT	fibrinolytic and thrombin inhibiting activities, for treating cardiac and			
PT	cerebral infarcct, pulmonary embolism, etc.			
XX				
PS	Example 1, Page 11 and Fig 1, 34pp; German.			
XX				
CC	Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1			
CC	are claimed (see features table). Sequences AAR66244-R66266 are specific			
CC	examples of such derive, which have both improved fibrinolytic and			
CC	thrombin-inhibiting activities, compared to known plasminogen activators			
CC	or thrombin inhibitors. The proteins are useful as thrombolytic agents,			
CC	e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac			
CC	and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003			
CC	to correct PN field.)			
XX				
XX				
SO	Sequence 386 AA;			
	Query Match	100.0%;	Score 44;	DB 2; Length 386;
	Best Local Similarity	100.0%;	Pred. No. 97;	
	Matches 8;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
OY				
	1 KPSSPPEE 8			
DB	90 KPSSPPEE 97			
	RESULT 22			
ID	AAW13636			
	AAW13636 standard; protein; 389 AA.			
XX				
XX	AAW13636;			
XX				
DT	04-JUN-1997 (first entry)			
XX				
DE	Human prourokinase variant lacking EGF domain loops 1 and 2.			
XX				
KW	Human; prourokinase; hPUK; variant; half-life; increase; EGF;			
XX	epidermal growth factor domain; deletion; thrombolytic; fibrinolytic.			
OS	Homo sapiens.			
OS	Synthetic.			
XX				
XX				
FT	Key	Location/Qualifiers		
FT	Region	1..10		
		/note= "residues 1-10 of native hPUK"		
FT	Region	11..389		

FT /note= "residues 33-411 of native hPUK"
 FT Misc-difference 155
 FT /note= "corresponds to TAC codon"
 XX
 XX EP398361-A.
 XX
 PD 22-NOV-1990.
 XX
 XX 18-MAY-1990; 90EP-00109472.
 XX
 PR 18-MAY-1989; 89JP-00126433.
 PR 22-FEB-1990; 90JP-00042020.
 XX
 PA (GREG) GREEN CROSS CORP.
 XX
 PI Tanabe T, Amatsuji Y, Kasai S, Hirose M, Morita M, Kawabe H,
 PI Airmura H;
 XX
 DR WPI; 1990-350146/47.
 DR N-PSDB; AAT61673.
 XX
 PT Human pro-urokinase variants - deficient in loop regions of epidermal
 XX growth factor, showing long blood half-life, as fibrinolytic agent.
 XX
 PS Claim 6; Page; 22pp; English.
 XX
 CC New variants of human prourokinase (hPUK) comprise a hPUK deficient in
 CC (i) at least part of the first loop region of the epidermal growth factor
 CC (EGF) domain; (ii) at least part of the first loop and at least part of
 CC the second loop; or (iii) at least part of the third loop. The hPUK
 CC variants show an increased blood half-life comparable to that of the
 CC whole EGF domain-deficient hPUK variant and urokinase while retaining the
 CC same properties as those of hPUK. They have potent thrombolytic activity
 CC and very little tendency to cause spontaneous bleeding. The present
 CC sequence represents a specific variant of hPUK which lacks loops 1 and 2
 CC of the EGF domain; the sequence does not appear in the specification and
 CC has been created using the wild-type hPUK sequence and the junction
 CC sequence after deletion, both of which are given (in Fig 1 and on page 8,
 CC respectively)
 XX
 SQ Sequence 389 AA;
 Query Match 100.0%; Score 44; DB 2; Length 389;
 Best Local Similarity 100.0%; Pred. No. 98;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSSPPE 8
 DB 114 KPSSPPE 121
 RESULT 23
 AAR66245
 ID AAR66245 standard; protein; 390 AA.
 XX
 AC AAR66245;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-AUG-1995 (first entry)
 XX
 DE Bifunctional urokinase variant M12.
 XX
 KM fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
 KM urokinase; variant; mucin.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..365
 FT /label= M4
 FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
 FT Disulfide-bond 4..85
 FT Disulfide-bond 25..67

FT Disulfide-bond 56..80
 FT Disulfide-bond 102..233
 FT Disulfide-bond 143..159
 FT Disulfide-bond 151..222
 FT Disulfide-bond 247..316
 FT Disulfide-bond 279..295
 FT Disulfide-bond 306..334
 FT Disulfide-bond 366..371
 FT Region /label= X1
 FT 372..390
 FT /label= Y1
 XX
 PN DE4323754-Cl.
 PD 01-DEC-1994.
 XX
 XX 15-JUL-1993; 93DE-04323754.
 XX
 PR 15-JUL-1993; 93DE-04323754.
 XX
 PA (CHER) GRUENTHAL GMBH.
 XX
 PI Steffens GJ, Whendt S, Schneider J, Heinzel-Wieland R;
 PI Saunders DJ;
 XX
 DR WPI; 1995-015191/03.
 XX
 PT New bifunctional urokinase derivs and related plasmids - with improved
 PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
 PT cerebral infarct, pulmonary embolism, etc.
 XX
 PS Example 1; Page 10 and Fig 1; 34pp; German.
 XX
 CC Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
 CC are claimed (see features table). Sequences AAR66244-R66266 are specific
 CC examples of such derivs. which have both improved fibrinolytic and
 CC thrombin-inhibiting activities, compared to known plasminogen activators
 CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
 CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
 CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX
 SQ Sequence 390 AA;
 Query Match 100.0%; Score 44; DB 2; Length 390;
 Best Local Similarity 100.0%; Pred. No. 98;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSSPPE 8
 DB 90 KPSSPPE 97
 RESULT 24
 AAR66247
 ID AAR66247 standard; protein; 390 AA.
 XX
 AC AAR66247;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-AUG-1995 (first entry)
 XX
 DE Bifunctional urokinase variant M14.
 XX
 KM fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
 KM urokinase; variant; mucin.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..365
 FT /label= M4
 FT /note= "unglycosylated prourokinase(Ser47-Leu411)"

FT	Disulfide-bond	4.	.85
FT	Disulfide-bond	25.	.67
FT	Disulfide-bond	56.	.80
FT	Disulfide-bond	102.	.233
FT	Disulfide-bond	143.	.159
FT	Disulfide-bond	151.	.222
FT	Disulfide-bond	247.	.316
FT	Disulfide-bond	279.	.295
FT	Disulfide-bond	306.	.334
FT	Disulfide-bond	366.	.371
FT	Region	/label= X1	
FT	Region	372.	.390
FT	Region	/label= Y1	
XX			
PN	DE4323754-C1.		
XX			
PD	01-DEC-1994.		
XX			
PF	15-JUL-1993;	93DE-04323754.	
XX			
PR	15-JUL-1993;	93DE-04323754.	
XX			
PA	(CHEF) GRUNENTHAL GMBH.		
PI	Steffens GJ, Wnendt S, Schneider J, Heinzl-Wieland R;		
PI	Saunders DJ;		
XX			
DR	WPI; 1995-015191/03.		
XX			
PT	New bifunctional urokinase derivs and related plasmids - with improved		
PT	fibrinolytic and thrombin inhibiting activities, for treating cardiac and		
PT	cerebral infarct, pulmonary embolism, etc.		
XX			
XX	Example 1; Page 10 and Fig 1; 34pp; German.		
CC	Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1		
CC	are claimed (see features table). Sequences AAR66244-R66266 are specific		
CC	examples of such derivs. which have both improved fibrinolytic and		
CC	thrombin-inhibiting activities, compared to known plasminogen activators		
CC	or thrombin inhibitors. The proteins are useful as thrombolytic agents,		
CC	e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac		
CC	and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003		
CC	to correct PN field.)		
XX			
SQ	Sequence 390 AA;		
Query Match		100.0%; Score 44; DB 2; Length 390;	
Best Local Similarity		100.0%; Pred. No. 98;	
Matches	8; Conservative	0; Mismatches	0; Indels
			Gaps 0;
QY	1 KPSSPPEE 8		
Db	90 KPSSPPEE 97		
RESULT 25			
AAR66260	AAR66260 standard; protein; 392 AA.		
XX			
AC	AAR66260;		
XX			
DT	25-MAR-2003 (revised)		
DT	17-AUG-1995 (first entry)		
XX			
DE	Bifunctional urokinase variant M27.		
XX			
KM	fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;		
XX	urokinase; variant; mutein.		
XX			
OS	Synthetic.		
XX			
Key		Location/Qualifiers	
FT	Region	1..365	

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FT FT /label= M4
FT FT /note= "unglycosylated prourokinase(Seif47-Leu411)"
FT FT Disulfide-bond 4. .85
FT FT Disulfide-bond 25. .67
FT FT Disulfide-bond 56. .80
FT FT Disulfide-bond 102. .233
FT FT Disulfide-bond 143. .159
FT FT Disulfide-bond 151. .222
FT FT Disulfide-bond 247. .316
FT FT Disulfide-bond 279. .295
FT FT Disulfide-bond 306. .334
FT FT Disulfide-bond 366. .371
FT FT Region /label= X1
FT FT Region /label= Y1
FT FT
XX XX DE4323754-CI.
XX XX 01-DEC-1994.
XX PD
XX PP 15-JUL-1993; 93DE-04323754.
XX PR 15-JUL-1993; 93DE-04323754.
XX PA (CHEF ) GRUENENTHAL GMBH.
XX PI Steffens GJ, Wendt S, Schneider J, Heinzel-Wieland R;
PI Saunders DJ;
XX DR WPI; 1995-015191/03.
XX PS
XX PT New bifunctional urokinase derivs and related plasmids - with improved
PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
PT cerebral infarct, pulmonary embolism, etc.
XX
PS Example 1; Page 11 and Fig 1; 34pp; German.
CC CC Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
CC CC are claimed (see features table). Sequences AAR6264-R6266 are specific
CC examples of such derivs. which have both improved fibrinolytic and
CC chrombin-inhibiting activities, compared to known plasminogen activators
CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
CC to correct PN field.)
CC CC
SQ Sequence. 392 AA;
Query Match 100.0%; Score 44; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KPSSPPEE 8
Db |||||
90 KPSSPPEE 97
RESULT 26
AAR6264
ID AAR6264 standard; protein; 392 AA.
XX
XX AAR6264;
XX AC
XX DT 25-MAR-2003 (revised)
XX DT 17-AUG-1995 (first entry)
XX DE 'Bifunctional urokinase variant M31.
XX KM fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
XX KW urokinase; variant; mutein.
XX OS Synthetic.
XX
```



```

FH Key location/Qualifiers
FT Region 1. .365
FT /label= M4
FT /note= "unglycosylated_prourokinase(Ser47-Leu411)"
FT Disulfide-bond 4. .85
FT Disulfide-bond 25. .67
FT Disulfide-bond 56. .80
FT Disulfide-bond 102. .233
FT Disulfide-bond 143. .159
FT Disulfide-bond 151. .222
FT Disulfide-bond 247. .316
FT Disulfide-bond 279. .295
FT Disulfide-bond 306. .334
FT Region 366. .371
FT /label= X1
FT Region 372. .392
FT /label= Y1
XX
XX DE4323754-C1.
XX
XX 01-DEC-1994.
XX
XX 15-JUL-1993; 93DE-04323754.
XX
XX 15-JUL-1993; 93DE-04323754.
XX
XX (CHEP ) GRUENENTHAL GMBH.
XX
XX Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;
XX Saunders DJ;
XX
XX WPI; 1995-015191/03.
DR
XX
XX New bifunctional urokinase derivs and related plasmids - with improved
XX fibrinolytic and thrombin inhibiting activities, for treating cardiac and
XX cerebral infarct, pulmonary embolism, etc.
XX
XX Example 1; Page 11 and Fig 1; 34pp; German.
XX
XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
XX are claimed (see features table). Sequences AAR66244-R66266 are specific
XX examples of such derivs. which have both improved fibrinolytic and
XX thrombin-inhibiting activities, compared to known plasminogen activators
XX or thrombin inhibitors. The proteins are useful as thrombolytic agents,
XX e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
XX and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
XX to correct FN field.)
XX
XX
XX Sequence 392 AA;
SQ
XX
XX Query Match 100.0%; Score 44; DB 2; Length 392;
XX Best Local Similarity 100.0%; Pred. No. 98;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 KPSSPPE 8
XX |||||
XX |||||
XX
XX Db 90 KPSSPPE 97
XX
RESULT 27
AAR6255
ID AAR6255 standard; protein; 392 AA.
XX
XX AAR6255;
XX
XX 25-MAR-2003 (revised)
XX 17-AUG-1995 (first entry)
XX
XX Bifunctional urokinase variant M22.
XX
XX fibrinolytic; thrombin inhibition; thrombolytic; anti-thrombotic;
XX urokinase; variant; mutein.
XX

```

OS	Synthetic.	Location/Qualifiers
XX	Key	1..365
XX	Region	/label= M4
FT		/note= "unglycosylated prourokinase (Ser47-Leu411)"
FT	Diulfide-bond	4..85
FT	Diulfide-bond	25..67
FT	Diulfide-bond	56..80
FT	Diulfide-bond	102..233
FT	Diulfide-bond	143..159
FT	Diulfide-bond	151..222
FT	Diulfide-bond	247..316
FT	Diulfide-bond	279..295
FT	Diulfide-bond	306..334
FT	Diulfide-bond	366..371
FT	Region	/label= X1
FT		372..392
FT		/label= Y1
XX	DE4323754-C1.	
XX	01-DEC-1994.	
XX	15-JUL-1993;	93DE-04323754.
XX	15-JUL-1993;	93DE-04323754.
XX	(CHBP) GRUENTHAL GMBH.	
XX	Steffens GJ, Wendt S, Schneider J, Heinzel-Wieland R, Saunders DJ;	
XX	WPI; 1995-015191/03.	
XX	New bifunctional urokinase derive and related plasmids - with improved fibrinolytic and thrombin inhibiting activities, for treating cardiac and cerebral infarct, pulmonary embolism, etc.	
XX	Example 1; Page 10 and Fig 1; 34pp; German.	
XX	Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1 are claimed (see features table). Sequences AAR6244-R6266 are specific examples of such derive. which have both improved fibrinolytic and thrombin-inhibiting activities, compared to known plasminogen activators or thrombin inhibitors. The proteins are useful as thrombolytic agents, e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003 to correct FN field.)	
XX	Sequence 392 AA;	
XX		
XX	Query Match	100.0%; Score 44; DB 2; Length 392;
XX	Best Local Similarity	100.0%; Pred. No. 98;
XX	Matches 8; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
XX	1 KPSSPPEE 8	
XX		
XX	90 KPSSPPEE 97	
XX	RESULT 28	
XX	AAR6259	
XX	AAR6259 standard; protein; 392 AA.	
XX	AAR6259;	
XX	25-MAR-2003 (revised)	
XX	17-AUG-1995 (first entry)	
XX	Bifunctional urokinase variant M26.	
XX	fibrinolytic;thrombin inhibition; thrombolytic; anti-thrombotic;	

KM	urokinase; variant; mutein.	
XX	Synthetic.	
OS		
XX	Key	Location/Qualifiers
FT	Region	1. .365 /label= M4
FT		/note= "unglycosylated prourokinase (Ser47-Leu411)"
FT	Disulfide-bond	4. .85
FT	Disulfide-bond	25. .67
FT	Disulfide-bond	56. .80
FT	Disulfide-bond	102. .233
FT	Disulfide-bond	143. .159
FT	Disulfide-bond	151. .222
FT	Disulfide-bond	247. .316
FT	Disulfide-bond	279. .295
FT	Disulfide-bond	306. .334
FT	Region	366. .371
FT	Region	/label= X1
FT		372. .392
FT		/label= Y1
XX		
XX	DE4323754-C1.	
XX		
PD	01-DEC-1994.	
XX		
PE	15-JUL-1993;	93DE-04323754.
XX		
PR	15-JUL-1993;	93DE-04323754.
XX		
PA	(CHEF) GRUNENTHAL GMBH.	
XX		
PI	Steffens GJ, Wendt S, Schneider J, Heinzel-Wieland R,	
PI	Saunders DJ;	
XX		
DR	WPI; 1995-015191/03.	
XX		
PT	New bifunctional urokinase derivs and related plaemids - with improved	
PT	fibrinolytic and thrombin inhibiting activities, for treating cardiac and	
PT	cerebral infarct, pulmonary embolism, etc.	
XX		
PS	Example 1; Page 11 and Fig 1; 34pp; German.	
XX		
CC	Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1	
CC	are claimed (see features table). Sequences AAR66244-R66266 are specific	
CC	examples of such derivs. which have both improved fibrinolytic and	
CC	thrombin-inhibiting activities, compared to known plasminogen activators	
CC	or thrombin inhibitors. The proteins are useful as thrombolytic agents,	
CC	e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac	
CC	and cerebral infarction and pulmonary embolism. (updated on 25-MAR-2003	
CC	to correct PN field.)	
SQ	Sequence 392 AA;	
Query Match	100.0%; Score 44; DB 2; Length 392;	
Best Local Similarity	100.0%; Pred. No. 98;	
Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 KPSSPPER 8	
DB	90 KPSSPPER 97	
RESULT 29		
AAR66261		
ID	AAR66261 standard; protein; 392 AA.	
XX		
AC	AAR66261;	
XX		
DT	25-MAR-2003 (revised)	
DT	17-AUG-1995 (first entry)	
DE	Bifunctional urokinase variant M28.	

XX	fibrinolytic; thrombin inhibition; thrombolytic; anti-thrombotic;
KW	urokinase; variant; mutein.
XX	
OS	Synthetic.
XX	
FH	Key
FT	Region
FT	Location/Qualifiers
FT	1..365
FT	/label= M4
FT	/note= "unglycosylated prourokinase (Ser47-Leu411) "
FT	
FT	Disulfide-bond
FT	4..85
FT	Disulfide-bond
FT	25..67
FT	Disulfide-bond
FT	56..80
FT	Disulfide-bond
FT	102..233
FT	Disulfide-bond
FT	143..159
FT	Disulfide-bond
FT	151..222
FT	Disulfide-bond
FT	247..316
FT	Disulfide-bond
FT	279..295
FT	Disulfide-bond
FT	306..334
FT	Disulfide-bond
FT	366..371
FT	Region
FT	/label= X1
FT	372..392
FT	/label= Y1
XX	
FN	DE4323754-C1.
XX	
PD	01-DEC-1994.
XX	
PE	15-JUL-1993; 93DE-04323754.
XX	
PR	15-JUL-1993; 93DE-04323754.
XX	
PA	(CHEF) GRUENENTHAL GMBH.
XX	
PI	Steffens GJ, Wendt S, Schneider J, Heinzel-Wieland R;
PI	Saunders DJ;
XX	
DR	WPI; 1995-015191/03.
XX	
PT	New bifunctional urokinase derivs and related plaemids - with improved
PT	fibrinolytic and thrombin inhibiting activities, for treating cardiac and
PT	cerebral infarct, pulmonary embolism, etc.
XX	
PS	Example 1; Page 11 and Fig 1; 34pp; German.
XX	
CC	Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
CC	are claimed (see features table). Sequences AAR66244-R66266 are specific
CC	examples of such derivs, which have both improved fibrinolytic and
CC	thrombin-inhibiting activities, compared to known plasminogen activators
CC	or thrombin inhibitors. The proteins are useful as thrombolytic agents,
CC	e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
CC	and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
CC	to correct PW field.)
XX	
SQ	Sequence 392 AA;
XX	
QY	Query Match 100.0%; Score 44; DB 2; Length 392;
XX	Best Local Similarity 100.0%; Pred. NO. 98;
DB	Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX	
QY	1 KPSSPPEE 8
XX	
DB	90 KPSSPPEE 97
XX	
RESULT 30	
ID	AAR66258
XX	AAR66258 standard; protein; 392 AA.
XX	
XX	AAR66258;
XX	
DT	25-MAR-2003 (revised)
DT	17-AUG-1995 (first entry)

```

XX DE Bifunctional urokinase variant M25.
XX KM fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
XX KM urokinase; variant; mutein.
XX OS Synthetic.
XX FH Key
XX FH Region
XX FT Location/Qualifiers
XX FT /label= M4
XX FT /note= "unglycosylated prourokinase (Ser47-Leu411)"
XX FT Disulfide-bond 4. .85
XX FT Disulfide-bond 25. .67
XX FT Disulfide-bond 56. .80
XX FT Disulfide-bond 102. .233
XX FT Disulfide-bond 143. .159
XX FT Disulfide-bond 151. .222
XX FT Disulfide-bond 247. .316
XX FT Disulfide-bond 279. .295
XX FT Disulfide-bond 306. .334
XX FT Disulfide-bond 366. .371
XX FT Region
XX FT /label= X1
XX FT /label= X1
XX FT Region
XX FT /label= Y1
XX PN DE4323754-Cl.
XX PD 01-DEC-1994.
XX PF 15-JUL-1993; 93DE-04323754.
XX PR 15-JUL-1993; 93DE-04323754.
XX PA (CHEF ) GRUENENTHAL GMBH.
XX PI Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;
XX PI Saunders DJ;
XX PI WPI; 1995-015191/03.
XX DR
XX XX New bifunctional urokinase derivs and related plasmids - with improved
XX PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
XX PT cerebral infarct, pulmonary embolism, etc.
XX PT Example 1; Page 11 and Fig 1; 34pp; German.
XX PS
XX XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
XX CC are claimed (see features table). Sequences AAR66244-R66266 are specific
XX CC examples of such derivs. which have both improved fibrinolytic and
XX CC thrombin-inhibiting activities, compared to known plasminogen activators
XX CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
XX CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
XX CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
XX CC to correct PN field.)
XX CC
XX SQ Sequence 392 AA;

Query Match 100.0%; Score 44; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSSPPEE 8
DB 90 KPSSPPEE 97

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DT 25-MAR-2003 (revised)
DT 17-AUG-1995 (first entry)
XX DE Bifunctional urokinase variant M30.
XX KM fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
XX KM urokinase; variant; mutein.
XX OS Synthetic.
XX FH Key
XX FH Region
XX FT Location/Qualifiers
XX FT /label= M4
XX FT /note= "unglycosylated prourokinase (Ser47-Leu411)"
XX FT Disulfide-bond 4. .85
XX FT Disulfide-bond 25. .67
XX FT Disulfide-bond 56. .80
XX FT Disulfide-bond 102. .233
XX FT Disulfide-bond 143. .159
XX FT Disulfide-bond 151. .222
XX FT Disulfide-bond 247. .316
XX FT Disulfide-bond 279. .295
XX FT Disulfide-bond 306. .334
XX FT Disulfide-bond 366. .371
XX FT Region
XX FT /label= X1
XX FT /label= X1
XX FT Region
XX FT /label= Y1
XX PN DE4323754-Cl.
XX PD 01-DEC-1994.
XX PF 15-JUL-1993; 93DE-04323754.
XX PR 15-JUL-1993; 93DE-04323754.
XX PA (CHEF ) GRUENENTHAL GMBH.
XX PI Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;
XX PI Saunders DJ;
XX PI WPI; 1995-015191/03.
XX DR
XX XX New bifunctional urokinase derivs and related plasmids - with improved
XX PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
XX PT cerebral infarct, pulmonary embolism, etc.
XX PT Example 1; Page 11 and Fig 1; 34pp; German.
XX PS
XX XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
XX CC are claimed (see features table). Sequences AAR66244-R66266 are specific
XX CC examples of such derivs. which have both improved fibrinolytic and
XX CC thrombin-inhibiting activities, compared to known plasminogen activators
XX CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
XX CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
XX CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
XX CC to correct PN field.)
XX CC
XX SQ Sequence 392 AA;

Query Match 100.0%; Score 44; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSSPPEE 8
DB 90 KPSSPPEE 97

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RESULT 31
 AAR66263
 ID AAR66263 standard; protein; 392 AA.
 XX AC AAR66263;
 XX

RESULT 32
 AAR66254
 ID AAR66254 standard; protein; 392 AA.
 XX

RESULT 34
 AAR66257
 ID AAR66257 standard; protein; 392 AA.
 AC AAR66257;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-AUG-1995 (first entry)
 XX
 DE Bifunctional urokinase variant M24.
 XX
 KW fibrinolysis; thrombin inhibition; chromolytic; anti-chromobotic;
 KM urokinase; variant; mutein.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Region
 FT
 FT Location/Qualifiers
 FT 1.365
 FT /label= M4
 FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
 FT
 FT Disulfide-bond 4..85
 FT Disulfide-bond 25..67
 FT Disulfide-bond 56..80
 FT Disulfide-bond 102..233
 FT Disulfide-bond 143..159
 FT Disulfide-bond 151..222
 FT Disulfide-bond 247..316
 FT Disulfide-bond 279..295
 FT Disulfide-bond 306..334
 FT Disulfide-bond 366..371
 FT Region
 FT /label= X1
 FT 372..392
 FT /label= Y1
 FT
 FT Region
 FT DE4323754-Cl.
 PN
 XX 01-DEC-1994.
 PD
 XX
 XX 15-JUL-1993; 93DE-04323754.
 PF
 XX 15-JUL-1993; 93DE-04323754.
 PR
 XX
 XX
 PA (CHER) GRUENTHAL GMBH.
 XX
 PI Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;
 PI Saunders DJ;
 PI
 DR WPI; 1995-015191/03.
 XX
 DR
 XX
 PT New bifunctional urokinase derivs and related plasmids - with improved
 PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
 PT cerebral infarct, pulmonary embolism, etc.
 PT
 PT
 XX
 PS Example 1; Page 11 and Fig 1; 34pp; German.
 XX
 XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
 CC are claimed (see features table). Sequences AAR66244-R66266 are specific
 CC examples of such derivs, which have both improved fibrinolytic and
 CC thrombin-inhibiting activities, compared to known plasminogen activators
 CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
 CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
 CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
 CC to correct PN field.)
 CC
 XX
 XX
 SQ Sequence 392 AA;
 XX
 Query Match 100.0%; Score 44; DB 2; Length 392;
 Best Local Similarity 100.0%; Pred. No. 98;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSSPPE 8
 DB 90 KPSSPPE 97

RESULT 35
 AAR66251
 ID AAR66251 standard; protein; 393 AA.
 AC AAR66251;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-AUG-1995 (first entry)
 XX
 DE Bifunctional urokinase variant M18.
 XX
 KW fibrinolysis; thrombin inhibition; chromolytic; anti-chromobotic;
 KM urokinase; variant; mutein.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Region
 FT
 FT Location/Qualifiers
 FT 1.365
 FT /label= M4
 FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
 FT
 FT Disulfide-bond 4..85
 FT Disulfide-bond 25..67
 FT Disulfide-bond 56..80
 FT Disulfide-bond 102..233
 FT Disulfide-bond 143..159
 FT Disulfide-bond 151..222
 FT Disulfide-bond 247..316
 FT Disulfide-bond 279..295
 FT Disulfide-bond 306..334
 FT Disulfide-bond 366..372
 FT Region
 FT /label= X1
 FT 373..393
 FT /label= Y1
 FT
 FT Region
 FT DE4323754-Cl.
 PN
 XX 01-DEC-1994.
 PD
 XX
 XX 15-JUL-1993; 93DE-04323754.
 PF
 XX 15-JUL-1993; 93DE-04323754.
 PR
 XX
 XX
 PA (CHER) GRUENTHAL GMBH.
 XX
 PI Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;
 PI Saunders DJ;
 PI
 DR WPI; 1995-015191/03.
 XX
 DR
 XX
 PT New bifunctional urokinase derivs and related plasmids - with improved
 PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
 PT cerebral infarct, pulmonary embolism, etc.
 PT
 PT
 XX
 PS Example 1; Page 10 and Fig 1; 34pp; German.
 XX
 XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
 CC are claimed (see features table). Sequences AAR66244-R66266 are specific
 CC examples of such derivs, which have both improved fibrinolytic and
 CC thrombin-inhibiting activities, compared to known plasminogen activators
 CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
 CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
 CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
 CC to correct PN field.)
 CC
 XX
 XX
 SQ Sequence 393 AA;
 XX
 Query Match 100.0%; Score 44; DB 2; Length 393;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSSPPE 8

XX Sequence 393 AA;
SQ

Query Match
Best Local Similarity 100.0%; Score 44; DB 2; Length 393;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
Db 90 KPSSPPEE 97

RESULT 40
AAR6250
ID AAR6250 standard; protein; 393 AA.
XX
AC AAR6250;
XX
DT 25-MAR-2003 (revised)
DT 17-AUG-1995 (first entry)
XX
DE Bifunctional urokinase variant M17.
XX
KM fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
KM urokinase; variant; muten.
XX
OS Synthetic.
XX
FH Key
FT Region
FT 1..365
FT /label= M4
FT /note="unglycosylated prourokinase(Ser47-Leu411)"
FT Disulfide-bond 4..85
FT Disulfide-bond 25..67
FT Disulfide-bond 56..80
FT Disulfide-bond 102..233
FT Disulfide-bond 143..159
FT Disulfide-bond 151..222
FT Disulfide-bond 247..316
FT Disulfide-bond 279..295
FT Disulfide-bond 306..334
FT 366..372
FT /label= X1
FT Region
FT 373..393
FT /label= Y1
XX
PN DE4323754-C1.
PD 01-DEC-1994.
XX
PF 15-JUL-1993; 93DE-04323754.
XX
PR 15-JUL-1993; 93DE-04323754.
XX
PA (CHEF) GRUENENTHAL GMBH.
XX
PI Steffens GJ, Wendt S, Schneider J, Heinzel-Wieland R;
PI Saunders DJ;
XX
DR WPI; 1995-015191/03.
XX
PT New bifunctional urokinase derivs and related plasmids - with improved
PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
PT cerebral infarct, pulmonary embolism, etc.
XX
PS Example 1; Page 10 and Fig 1; 34pp; German.
XX
CC Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
CC are claimed (see features table). Sequences AAR6244-R6266 are specific
CC examples of such derivs. which have both improved fibrinolytic and
CC thrombin-inhibiting activities, compared to known plasminogen activators
CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac

CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 393 AA;
XX

Query Match
Best Local Similarity 100.0%; Score 44; DB 2; Length 393;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
Db 90 KPSSPPEE 97

RESULT 41
AAR9597
ID AAR9597 standard; protein; 393 AA.
XX
AC AAR9597;
XX
DT 05-DEC-1996 (first entry)
DT
XX
DE Chimeric protein M38 encoded by pSEI.
XX
KM Thrombin; inhibition; thrombus; fibrinolysis; chimeric protein;
KM plasminogen activating sequence; fibrinolysis; infarction;
KM angina pectoris; deep vein thrombosis.
XX
OS Synthetic.
XX
PN EP714982-A2.
XX
PD 05-JUN-1996.
XX
PF 16-NOV-1995; 95EP-00118050.
XX
PR 30-NOV-1994; 94DE-04442665.
XX
PA (CHEF) GRUENENTHAL GMBH.
XX
PI Wendt S, Steffens GJ, Janocha E, Heinzel-Wieland R;
XX
DR WPI; 1996-269715/28.
XX
PT Chimeric protein contg. plasminogen activating sequence and thrombin-
PT inhibiting sequence - useful as thrombus-specific thrombolytic agent with
PT rapid action.
XX
PS Example 1; Page 21-22; 37pp; German.
XX
CC Example 1 describes the prodn. of plasmids pSEI and pSE9 contg. a DNA
CC encoding a chimeric protein with fibrinolytic and thrombin-inhibiting
CC properties. pSEI encodes the protein given in AAR9597 and pSE9 encodes
CC the protein given in AAR9596
XX
SQ Sequence 393 AA;
XX

Query Match
Best Local Similarity 100.0%; Score 44; DB 2; Length 393;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
Db 91 KPSSPPEE 98

RESULT 42
AAR9596
ID AAR9596 standard; protein; 393 AA.
XX
AC AAR9596;
XX
DT 05-DEC-1996 (first entry)

XX Chimeric protein M37 encoded by pSE9.
 DR Thrombin; inhibition; thrombus; thrombolysis; chimeric protein;
 XX plasminogen activating sequence; fibrinolysis; infarction;
 KW angina pectoris; deep vein thrombosis.
 XX Synthetic.
 OS
 XX EP714982-A2.
 PN
 XX 05-JUN-1996.
 PD
 XX 16-NOV-1995; 95EP-00118050.
 PF
 XX 30-NOV-1994; 94DE-04442665.
 PR
 XX (CHEP) GRUENENTHAL GMBH.
 PA
 XX Wnendt S, Steffens GJ, Janocha E, Heinzel-Wieland R;
 PI WPI; 1996-269715/28.
 DR
 XX Chimeric protein contg. plasminogen activating sequence and thrombin-
 PT inhibiting sequence - useful as thrombus-specific thrombolytic agent with
 PT rapid action.
 PS Example 1; Page 19-20; 37pp; German.
 CC Example 1 describes the prodn. of plasmin pSE1 and pSE9 contg. a DNA
 CC encoding a chimeric protein with fibrinolytic and thrombin-inhibiting
 CC properties. pSE1 encodes the protein given in AAR99597 and pSE9 encodes
 CC the protein given in AAR99596
 SQ Sequence 393 AA;
 Query Match 100.0%; Score 44; DB 2; Length 393;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSSPPEE 8
 DB 91 KPSSPPEE 98
 RESULT 43
 AAR99885
 ID AAR99885 standard; peptide; 393 AA.
 XX
 AC AAR99885;
 XX
 XX 27-JUN-1997 (first entry)
 DT
 XX M36: fibrinolytic and anticoagulant activity contg. protein.
 DE
 XX Thrombin; factor Xa; anticoagulant; thrombolytic; plasminogen; urokinase;
 KW activator; streptokinase; staphylokinase; APSAC;
 KW antisolated plasminogen streptokinase activator complex; hirudin;
 KW hirudin; antistatin; pMUT27; pMS1; pSE8; pMS56.
 XX
 OS Synthetic.
 XX
 XX EP712934-A2.
 PN
 XX 22-MAY-1996.
 PD
 XX 03-NOV-1995; 95EP-00117316.
 PF
 XX 17-NOV-1994; 94DE-04440892.
 PR
 XX (CHEP) GRUENENTHAL GMBH.
 PA
 XX Wnendt S, Heinzel-Wieland R, Steffens GJ,
 PI

XX WPI; 1996-240720/25.
 DR
 XX Proteins with fibrinolytic and anticoagulant activity - useful as
 PT thrombolytic agents.
 PT
 XX Disclosure; Fig 18; 59pp; German.
 PS
 XX New peptide (I) with fibrinolytic and anticoagulant activity comprise a
 CC plasminogen-activating amino acid sequence (A) fused at the N- and/or C-
 CC terminus to a thrombin and/or factor Xa inhibiting amino acid sequence
 CC (B). Excluded from the claims are (I) where (A) is Ser47 to Leu411 of
 CC unglycosylated urokinase linked at the C-terminus to sequences (i) to
 CC (iii): T1-RE-T2-GGNGNDPEFEIPEYL-T3 (i) T1-REPLRNPDKYEPWEDERKHE (ii)
 CC T1-RPSRPEREIEDEER (iii) where T1 = P or V; T2 = L or a bond; T3 = O or
 CC OH. (A) is pref. (pro)urokinase, tissue plasminogen activator (tPA), bat-
 CC PA (all opt. modified by deletion, substitution, insertion and/or addn.);
 CC streptokinase; staphylokinase; and/or APSAC (antisolated plasminogen
 CC streptokinase activator complex), esp. prourokinase (411 amino acids) or
 CC its Ser47 to Leu411 or Ser138 to Leu411 fragments, or t-PA (527 amino
 CC acids) or its Ser99Arg to 527Pro or 174Ser to 527Pro fragments. (B) has
 CC hirudin or hirudin activities; or is derived from the human thrombin
 CC receptor, antistatin and/or the tick anticoagulant peptide. Most pref.
 CC are the 65 amino acid hirudin sequence or one of the six sequences given
 CC in AAR99879 to AAR99884. Plasmids pMUT27 (MS1), pMS1 (MS112), pSE8 (M36)
 CC and pMS6 (M43) contain the sequences encoding AAR99885 to AAR99888,
 CC respectively. The products were tested in human citrated plasma (5 microg
 CC in 200 microl 1:10 diluted plasma). The thrombin time was then 1.2, 3,
 CC 2.8 and 1.2 times greater, respectively, than in the absence of the
 CC product
 SQ Sequence 393 AA;
 Query Match 100.0%; Score 44; DB 2; Length 393;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSSPPEE 8
 DB 91 KPSSPPEE 98
 RESULT 44
 AAR47902
 ID AAR47902 standard; protein; 395 AA.
 XX
 AC AAR47902;
 XX
 XX 13-JUL-1994 (first entry)
 DT
 XX Pro-urokinase derivative.
 DE
 XX Pro-urokinase derivative.
 XX
 XX Pro-urokinase; half-life; thrombolytic; thrombosis; fibrinolytic; factor.
 KW
 XX Homo sapiens.
 OS
 XX JP05336965-A.
 PN
 XX 21-DEC-1993.
 PD
 XX 17-OCT-1991; 91JP-00269615.
 PF
 XX 17-OCT-1991; 91JP-00269615.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX WPI; 1994-030907/04.
 DR
 XX N-PSDB; AA055771.
 PT
 XX Novel human pro-urokinase deriva. having long half-life - with high
 PT thrombolytic activity, useful for treatment of thrombosis.
 PS Disclosure; Page 14; 29pp; Japanese.

XX Sequences (AA055771-72) are pro-urokinase derivatives. The products have
 CC an inserted sugar moiety having an amino acid substituted, depleted or
 CC inserted amino around the thrombin cleavage site. They also have a long
 CC half-life allowing them to be used in the treatment of thrombosis
 XX
 SQ Sequence 395 AA;

Query Match 100.0%; Score 44; DB 2; Length 395;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
 |||||
 Db 120 KPSSPPE 127

RESULT 45

AA066265
 ID AAR66265 standard; protein; 395 AA.

AC AAR66265;

DT 25-MAR-2003 (revised)
 DT 17-AUG-1995 (first entry)

DE Bifunctional urokinase variant M32.

KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
 KM urokinase; variant; mutein.

OS Synthetic.

Key Location/Qualifiers
 Region 1..365
 /label= M4
 /note= "unglycosylated prourokinase (Ser47-Leu411)"

FT Disulfide-bond 4..85
 FT Disulfide-bond 25..67
 FT Disulfide-bond 56..80
 FT Disulfide-bond 102..233
 FT Disulfide-bond 143..159
 FT Disulfide-bond 151..222
 FT Disulfide-bond 247..316
 FT Disulfide-bond 279..295
 FT Disulfide-bond 306..334
 FT Disulfide-bond 366..371
 FT Region /label= X1
 FT 372..395
 FT Region /label= Y1

DE4323754-C1.

PD 01-DEC-1994.

PF 15-JUL-1993; 93DE-04323754.

PR 15-JUL-1993; 93DE-04323754.

XX (CHEP) GRUENENTHAL GMBH.

PI Steffens GJ, Wendt S, Schneider J, Heinzel-Wieland R;
 PI Saunders DJ;

DR WPI; 1995-015191/03.

XX New bifunctional urokinase derivs and related plasmids - with improved
 PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
 PT cerebral infarct, pulmonary embolism, etc.

XX Example 1; Page 11 and Fig 1; 34pp; German.

PS Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1

CC are claimed (see features table). Sequences AAR66264-R66266 are specific
 CC examples of such derivs. which have both improved fibrinolytic and
 CC thrombin-inhibiting activities, compared to known plasminogen activators
 CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
 CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
 CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
 CC to correct FN field.)
 XX

SQ Sequence 395 AA;

Query Match 100.0%; Score 44; DB 2; Length 395;
 Best Local Similarity 100.0%; Pred. No. 99;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
 |||||
 Db 90 KPSSPPE 97

RESULT 46

AA066262
 ID AAR66262 standard; protein; 395 AA.

AC AAR66262;

DT 25-MAR-2003 (revised)
 DT 17-AUG-1995 (first entry)

DE Bifunctional urokinase variant M29.

KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
 KM urokinase; variant; mutein.

OS Synthetic.

Key Location/Qualifiers
 Region 1..365
 /label= M4
 /note= "unglycosylated prourokinase (Ser47-Leu411)"

FT Disulfide-bond 4..85
 FT Disulfide-bond 25..67
 FT Disulfide-bond 56..80
 FT Disulfide-bond 102..233
 FT Disulfide-bond 143..159
 FT Disulfide-bond 151..222
 FT Disulfide-bond 247..316
 FT Disulfide-bond 279..295
 FT Disulfide-bond 306..334
 FT Disulfide-bond 366..371
 FT Region /label= X1
 FT 372..395
 FT Region /label= Y1

DE4323754-C1.

PD 01-DEC-1994.

PF 15-JUL-1993; 93DE-04323754.

PR 15-JUL-1993; 93DE-04323754.

XX (CHEP) GRUENENTHAL GMBH.

PI Steffens GJ, Wendt S, Schneider J, Heinzel-Wieland R;
 PI Saunders DJ;

DR WPI; 1995-015191/03.

XX New bifunctional urokinase derivs and related plasmids - with improved
 PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
 PT cerebral infarct, pulmonary embolism, etc.

XX Example 1; Page 11 and Fig 1; 34pp; German.

XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
 CC are claimed (see features table). Sequences AAR66244-R66266 are specific
 CC examples of such derivs. which have both improved fibrinolytic and
 CC thrombin-inhibiting activities, compared to known plasminogen activators
 CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
 CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
 CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
 CC to correct PN field.)

XX Sequence 395 AA;

Query Match 100.0%; Score 44; DB 2; Length 395;

Best Local Similarity 100.0%; Pred. No. 99;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSSPPEE 8
 |||||
 DB 90 KPSSPPEE 97

RESULT 47

AAR66246
 ID AAR66246 standard; protein; 396 AA.

AC AAR66246;

DT 25-MAR-2003 (revised)
 DT 17-AUG-1995 (first entry)

DE Bifunctional urokinase variant M13.

XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
 KW urokinase; variant; mutain.

XX Synthetic.

OS Key Location/Qualifiers

FT Region 1..365 /label= M4

FT Disulfide-bond 4..85 /note= "unglycosylated prourokinase(Ser47-Leu411)"

FT Disulfide-bond 25..67

FT Disulfide-bond 56..80

FT Disulfide-bond 102..233

FT Disulfide-bond 143..159

FT Disulfide-bond 151..222

FT Disulfide-bond 247..316

FT Disulfide-bond 279..295

FT Disulfide-bond 306..334

FT Region 366..377

FT /label= X1

FT 378..396

FT /label= Y1

DE4323754-Cl.

01-DEC-1994.

15-JUL-1993; 93DE-04323754.

15-JUL-1993; 93DE-04323754.

(CHRP) GRUENTHAL GMBH.

Steffens GJ, Wendt S, Schneider J, Heinzel-Melend R;

Saunders DJ;

WPI, 1995-015191/03.

New bifunctional urokinase derivs and related plasmids - with improved

fibrinolytic and thrombin inhibiting activities, for treating cardiac and

cerebral infarct, pulmonary embolism, etc.

XX Example 1; Page 10 and Fig 1; 34pp; German.

XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
 CC are claimed (see features table). Sequences AAR66244-R66266 are specific
 CC examples of such derivs. which have both improved fibrinolytic and
 CC thrombin-inhibiting activities, compared to known plasminogen activators
 CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
 CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
 CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
 CC to correct PN field.)

XX Sequence 396 AA;

Query Match 100.0%; Score 44; DB 2; Length 396;

Best Local Similarity 100.0%; Pred. No. 99;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSSPPEE 8
 |||||
 DB 90 KPSSPPEE 97

RESULT 48

AAR1828
 ID AAR1828 standard; protein; 397 AA.

AC AAR1828;

DT 08-JUL-1991 (first entry)

DE FB-FB-UK fusion conjugate.

XX Fibrin-binding protein; fibrinolysis; intravascular thrombi; fibrinogen;

KW urokinase; fusion protein.

XX Staphylococcus aureus.

OS Key Location/Qualifiers

FT Peptide 2..61 /label= FB monomer

FT Peptide 62..119 /label= FB monomer

FT Peptide 120 /label= linker

FT Peptide 121..397 /label= human urokinase-B chain

US5011686-A.

30-APR-1991.

15-NOV-1989; 89US-00437769.

21-SEP-1987; 87US-0009242.

(CREA-) CREATIVE BIOMOLEC.

Pang RHL;

WPI; 1991-140198/19.

N-PADB; AAO11650.

Imparting injectable fibrinolytic agent - with affinity for intravascular

thrombus, by linking agent to fibrin binding domain.

Disclosure; Fig 3; 18pp; English.

The conjugate comprises an FB-FB dimer linked via a Ser residue to the B

chain of human urokinase. The FB fragment has selective affinity for

fibrin, low affinity for fibrinogen, and minimal immunogenicity,

impacting thrombus-targeting capability. See also AAR1821 and AAR1829

Query Match 100.0%; Score 44; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 1e+02; 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
|||
Db 126 KPSSPPEE 133

Search completed: June 18, 2004, 12:58:45
Job time : 71 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 12:52:33 ; Search time 11 Seconds
(without alignments)
37.869 Million cell updates/sec

Title: US-10-655-201-2
Perfect score: 44
Sequence: 1 KXSPPEB 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	431	1 UROK_HUMAN	P00749 homo sapien
2	44	100.0	433	1 UROK_PAPCY	P16227 papio cynoc
3	36	81.8	418	1 PEDF_HUMAN	P36955 homo sapien
4	36	81.8	892	1 YB96_HUMAN	O96km6 homo sapien
5	36	81.8	1088	1 PIGO_HUMAN	O8te68 homo sapien
6	36	81.8	1358	1 SIR4_YEAST	P11978 saccharomyc
7	36	81.8	1806	1 CALB_HUMAN	P12107 homo sapien
8	35	79.5	249	1 IAP2_NPVAC	P41454 autographa
9	35	79.5	522	1 FINC_CANFA	O28275 canis fami
10	35	79.5	522	1 FINC_HORSE	O28377 equus cabal
11	35	79.5	754	1 ASRH_BOVIN	O28056 bos taurus
12	35	79.5	784	1 K6P_HUMAN	O01813 homo sapien
13	35	79.5	784	1 K6P_MOUSE	O9wua3 mus musculu
14	35	79.5	786	1 K6P_RAT	P47860 rattus norv
15	35	79.5	791	1 K6P_RABIT	P07918 herpes simp
16	35	79.5	1240	1 DPOL_HSV21	O9c0c2 homo sapien
17	35	79.5	1729	1 TABP_HUMAN	O9u1f9 homo sapien
18	35	79.5	1878	1 BAZA_HUMAN	P23468 homo sapien
19	35	79.5	1912	1 PTPD_HUMAN	O13332 homo sapien
20	35	79.5	1948	1 PTNS_HUMAN	O07589 bos taurus
21	35	79.5	2265	1 FINC_BOVIN	P02751 homo sapien
22	35	79.5	2386	1 FINC_MOUSE	P01276 mus musculu
23	35	79.5	2477	1 FINC_MOUSE	P04937 rattus norv
24	35	79.5	2477	1 FINC_RAT	P42776 arabisidops
25	34	77.3	382	1 GBR3_ARATH	P34960 mus musculu
26	34	77.3	462	1 MM12_MOUSE	P05887 human immu
27	34	77.3	499	1 GAG_HV1C4	P04591 human immu
28	34	77.3	499	1 GAG_HV1H2	P12464 human immu
29	34	77.3	499	1 GAG_HV1J3	O70623 human immu
30	34	77.3	499	1 GAG_HV1LW	P12463 human immu
31	34	77.3	499	1 GAG_HV1NS	P05890 human immu
32	34	77.3	500	1 GAG_HV1RH	P03349 human immu
33	34	77.3	501	1 GAG_HV1A2	

34	34	77.3	503	1 GAG_HV1JR	P20873 human immu
35	34	77.3	506	1 GAG_HV1BN	P05888 human immu
36	34	77.3	511	1 GAG_HV1B1	P03347 human immu
37	34	77.3	511	1 GAG_HV1B5	P04593 human immu
38	34	77.3	511	1 GAG_HV1B8	P03348 human immu
39	34	77.3	511	1 GAG_HV1BP	P03350 human immu
40	34	77.3	553	1 MIS_MOUSE	P49000 rattus norv
41	34	77.3	555	1 MIS_MOUSE	P27106 mus musculu
42	34	77.3	598	1 NR42_HUMAN	P43354 homo sapien
43	34	77.3	598	1 NR42_MOUSE	O06219 mus musculu
44	34	77.3	598	1 NR42_RAT	O07917 rattus norv
45	34	77.3	615	1 YJ13_SCHPO	O13681 schizosacch
46	34	77.3	886	1 CN4A_HUMAN	P27815 homo sapien
47	34	77.3	928	1 RSC1_YEAST	P53236 saccharomyc
48	34	77.3	959	1 G2D1_HUMAN	O9u1f9 h general t
49	34	77.3	1080	1 MREB_MOUSE	P59759 mus musculu
50	34	77.3	1088	1 MREB_HUMAN	O9u1f7 mus musculu
51	34	77.3	1104	1 G2D1_MOUSE	O13681 schizosacch
52	34	77.3	1567	1 RM1_DROME	P27815 homo sapien
53	33	75.0	153	1 GSPG_ERWCH	O9v7h4 drosophila
54	33	75.0	180	1 DADR_RABIT	P31585 erwina chr
55	33	75.0	245	1 PCYA_ANASP	O02664 ocytolaqus
56	33	75.0	366	1 CD44_BOVIN	O93cno anabaena sp
57	33	75.0	375	1 KORA_METTH	O29423 bos taurus
58	33	75.0	393	1 STAD_SOLCO	O27112 methanobact
59	33	75.0	397	1 DJA4_HUMAN	O41319 solanum com
60	33	75.0	397	1 DJA4_MOUSE	O8wz22 homo sapien
61	33	75.0	399	1 STAD_SPIOL	O9jnc3 mus musculu
62	33	75.0	411	1 IF2G_PPRAB	P28645 spiracle ol
63	33	75.0	411	1 IF2G_PPRAB	O9v1g0 pyrococcus
64	33	75.0	411	1 IF2G_PPRAB	O8u082 pyrococcus
65	33	75.0	424	1 IF2G_PPRAB	O59410 pyrococcus
66	33	75.0	506	1 GAG_SIVM1	O29663 archaeoglob
67	33	75.0	514	1 CSA_DICDI	P05894 simian immu
68	33	75.0	640	1 TERM_ADE07	P08796 dicystosteli
69	33	75.0	830	1 MCM2_SCHPO	P03270 human adeno
70	33	75.0	1093	1 PIGO_MOUSE	P40377 schizosacch
71	33	75.0	1097	1 KFLD_RAT	O9j316 mus musculu
72	33	75.0	1296	1 ASAI_ENTPA	P17953 rattus norv
73	33	75.0	3644	1 MINT_MOUSE	O62504 mus musculu
74	33	75.0	5262	1 MLG2_HUMAN	O14686 homo sapien
75	32	72.7	138	1 LACR_HUMAN	O9g2z8 homo sapien
76	32	72.7	145	1 SELM_HUMAN	O8wz22 homo sapien
77	32	72.7	145	1 SELM_MOUSE	O8vnc3 mus musculu
78	32	72.7	174	1 PTRY_SPIOL	P38365 spiracle ol
79	32	72.7	243	1 FCSE_RAT	P13386 rattus norv
80	32	72.7	243	1 NUKS_HUMAN	O9h1e3 homo sapien
81	32	72.7	247	1 SURE_CHRVO	O7nrv1 chromobacte
82	32	72.7	252	1 TRT3_COTJA	P06398 coturnix co
83	32	72.7	262	1 TRT3_CHICK	P12620 gallus gall
84	32	72.7	283	1 EXTN_SORBI	P24152 sorghum bic
85	32	72.7	377	1 SX18_MOUSE	P43680 mus musculu
86	32	72.7	420	1 SYS_THERT	P34945 therinus the
87	32	72.7	431	1 TOLB_YERPE	O8z9z1 yerinsula pe
88	32	72.7	446	1 PIV2_ADE40	P48752 human adeno
89	32	72.7	452	1 ETV6_HUMAN	P41312 homo sapien
90	32	72.7	475	1 RBL_PULAU	O43036 plumbago au
91	32	72.7	476	1 KE4_MOUSE	O31125 mus musculu
92	32	72.7	538	1 CN93_HUMAN	O9h912 homo sapien
93	32	72.7	539	1 Y793_TREPA	O81721 treponema p
94	32	72.7	549	1 TEGU_HCMV	P07387 human cytom
95	32	72.7	562	1 SVK_AERPE	O9v1f5 aeropyrum p
96	32	72.7	632	1 FANZ_HUMAN	O9v1f5 aeropyrum p
97	32	72.7	640	1 HKR1_HUMAN	P10072 homo sapien
98	32	72.7	652	1 CD93_HUMAN	O9npv3 homo sapien
99	32	72.7	685	1 SNK_HUMAN	O9npv3 homo sapien
100	32	72.7	783	1 YAYB_SCHPO	O10218 schizosacch
101	32	72.7	875	1 UBP7_SCHPO	O9p7b5 schizosacch
102	32	72.7	941	1 DNAB_PROMA	O30477 rhodothermu
103	32	72.7	953	1 LDM1_ARATH	O38796 arabidopsi
104	32	72.7	1130	1 SN3B_HUMAN	O75182 homo sapien
105	32	72.7	1234	1 JMD_MOUSE	O62315 mus musculu
106	32	72.7	1266	1 JMD_HUMAN	O92833 homo sapien

107	32	72.7	1281	1	IP3S_MOUSE	Q9329	mus musculus	180	31	70.5	805	1	TAC1_HUMAN	Q75410	homo sapien
108	32	72.7	1426	1	AI0D_HUMAN	Q9241	homo sapien	181	31	70.5	820	1	YNH4_CAEEL	P32742	caenorhabd1
109	32	72.7	12701	1	IP39S_RAT	P2995	rattus norv	182	31	70.5	860	1	AREA_PENRO	P13508	penicillium
110	32	72.7	3130	1	PD0Z_HUMAN	O6067	homo sapien	183	31	70.5	862	1	Z409_HUMAN	Q9296	homo sapien
111	31	70.5	78	1	YDZH_BACSU	O31496	baclillus su	184	31	70.5	865	1	NRA9_PENUR	Q92269	penicillium
112	31	70.5	82	1	HPIS_MARPU	P59860	marichromat	185	31	70.5	872	1	SCDS_YEAST	P34758	saccharomyc
113	31	70.5	83	1	HPIS_CHRGR	P00262	chromatium	186	31	70.5	911	1	CAPA_MOUSE	Q9QWU0	mus musculus
114	31	70.5	83	1	HPIS_THETI	P80176	thermochrom	187	31	70.5	911	1	PTP3_YEAST	P40048	saccharomyc
115	31	70.5	87	1	NXL4_BUNMU	O12961	bungarus mu	188	31	70.5	928	1	VGLE_HSVBC	P12640	bovine hepr
116	31	70.5	94	1	KV11_RABIT	P01662	oryctolagus	189	31	70.5	932	1	VGLE_HSVBC	P12640	bovine hepr
117	31	70.5	101	1	VF17_VAVU	P33875	variola vir	190	31	70.5	956	1	NU1I_MAGGR	O01168	magnaporthe
118	31	70.5	122	1	HPIS_CHRVT	P00260	chromatium	191	31	70.5	971	1	AREA_GIBFU	P78668	gibberella
119	31	70.5	127	1	LEC_GALNI	P30617	galactinus n	192	31	70.5	1034	1	ENTK_PIG	P98074	sus scrofa
120	31	70.5	165	1	GCSH_ARATH	P25855	arabidopsis	193	31	70.5	1036	1	NT12_NEUCR	P19212	neurospora
121	31	70.5	166	1	GCSI_ARATH	O91910	arabidopsis	194	31	70.5	1043	1	Y483_CHLPP	Q92828	chlamydia p
122	31	70.5	184	1	PEPI_HUMAN	O8N95	homo sapien	195	31	70.5	1132	1	YKKS_YEAST	P34250	saccharomyc
123	31	70.5	228	1	VSPA_LACMU	P33569	lachesia mu	196	31	70.5	1141	1	MYPE_HUMAN	O00872	homo sapien
124	31	70.5	227	1	YGHS_ECOLI	O46843	escherichia	197	31	70.5	1200	1	AT19_MOUSE	P59509	mus musculus
125	31	70.5	257	1	VSPC_TRIGA	O13062	trimeresuru	198	31	70.5	1389	1	LTHS_MOUSE	O8CG18	mus musculus
126	31	70.5	262	1	BGSX_ACEXY	O9W69	acetobacter	199	31	70.5	1427	1	ZFH2_HUMAN	Q9CG41	homo sapien
127	31	70.5	297	1	PEXC_DROME	O9VPS5	aceticobact	200	31	70.5	1440	1	SYEP_HUMAN	P07814	homo sapien
128	31	70.5	304	1	DPPC_BACPF	P43312	baclillus ps	201	31	70.5	1713	1	LTHL_MOUSE	O8CG19	mus musculus
129	31	70.5	307	1	COPE_BOVIN	O28104	bos taurus	202	31	70.5	1820	1	STP9_HUMAN	Q92D5	mus sapien
130	31	70.5	307	1	COPE_CRIGR	O60445	cricetulus	203	31	70.5	1942	1	HEI2_HUMAN	P42554	homo sapien
131	31	70.5	307	1	COPE_HUMAN	O14579	homo sapien	204	31	70.5	2065	1	T2D1_DROME	P51123	drosophila
132	31	70.5	311	1	ATH6_ARATH	P46668	arabidopsis	205	31	70.5	2763	1	TEGU_VZVD	P09278	varicella-z
133	31	70.5	314	1	YDQC_SCHPO	O14204	schizosach	206	31	70.5	2774	1	MAPA_RAT	P34926	rattus norv
134	31	70.5	316	1	APB_BOVIN	O03247	bos taurus	207	31	70.5	2805	1	MLI3_MOUSE	P78559	homo sapien
135	31	70.5	328	1	VMSA_HPBUD	P31345	duck hepati	208	31	70.5	4903	1	PCLO_MOUSE	O8BH4	mus musculus
136	31	70.5	329	1	GC3_MOUSE	P22436	mus musculus	209	31	70.5	5038	1	PCLO_MOUSE	Q9QX7	mus musculus
137	31	70.5	373	1	MEGI_HUMAN	Q9UB11	homo sapien	210	31	70.5	5085	1	PCLO_RAT	Q9JX86	rattus norv
138	31	70.5	377	1	STAD_GOSHI	O42770	gossypium h	211	31	70.5	5120	1	PCLO_CHICK	Q9P36	gallus gall
139	31	70.5	388	1	GC3M_MOUSE	P03987	mus musculus	212	31	70.5	5147	1	PCLO_HUMAN	O9Y670	homo sapien
140	31	70.5	398	1	STAD_BRANA	P29108	brassica na	213	31	68.2	48	1	RBL_PINS	P81080	pinus pinas
141	31	70.5	399	1	SP2_HUMAN	O81W5	homo sapien	214	31	68.2	53	1	RBL_MALDO	P31194	malus domes
142	31	70.5	405	1	GDFB_MOUSE	O92144	mus musculus	215	31	68.2	54	1	RBL_GEUBO	P31188	geum borisi
143	31	70.5	415	1	EF1G_YEAST	P29547	saccharomyc	216	31	68.2	54	1	RBL_ICAMA	P31190	icactina man
144	31	70.5	416	1	YHR5_YEAST	P38823	saccharomyc	217	31	68.2	54	1	RBL_ILEAQ	P31191	ilex aquilo
145	31	70.5	463	1	D2DR_FUGRU	P53437	fugu rubrip	218	31	68.2	54	1	RBL_ILECI	P31192	ilex aquilo
146	31	70.5	465	1	SNX8_HUMAN	O9Y5X2	homo sapien	219	31	68.2	54	1	RBL_ILEPE	O07049	ilex pernyi
147	31	70.5	480	1	DDC_CAVPO	P22781	cavia porce	220	31	68.2	54	1	RBL_MAGLI	P31193	magnolia il
148	31	70.5	480	1	IRXI_MOUSE	P81068	mus musculus	221	31	68.2	54	1	RBL_MERAN	P31195	mercurialis
149	31	70.5	480	1	KLPA_RAT	O08876	rattus norv	222	31	68.2	54	1	RBL_RHACA	P31198	thamnos cat
150	31	70.5	482	1	PO24_POPJA	O03275	popillia ja	223	31	68.2	54	1	RBL_RIBAM	P31199	ribes ameri
151	31	70.5	486	1	MEC2_HUMAN	P51608	homo sapien	224	31	68.2	57	1	RBL_BUXSE	P31180	buxus sempe
152	31	70.5	496	1	GTR3_CHICK	P28568	gallus gall	225	31	68.2	57	1	RBL_CAMSI	P31181	camellia si
153	31	70.5	505	1	FXO4_HUMAN	P98177	homo sapien	226	31	68.2	58	1	RBL_EUOBU	P31185	eunymus bu
154	31	70.5	520	1	RXR8_MOUSE	P28704	mus musculus	227	31	68.2	58	1	RBL_EUOMA	P31186	eunymus ma
155	31	70.5	527	1	GI9P_HUMAN	P14314	homo sapien	228	31	68.2	58	1	RBL_EUPCH	P31187	euphorbia c
156	31	70.5	534	1	APG_ARATH	P40602	arabidopsis	229	31	68.2	58	1	RBL_WEISY	P31200	weilmannia
157	31	70.5	572	1	CABF_MOUSE	Q94057	mus musculus	230	31	68.2	58	1	RBL_ROSDA	P31196	nemopanthus
158	31	70.5	575	1	TERM_ADEGI	O64752	aviana adeno	231	31	68.2	143	1	RBL_NEMMU	P50550	homo sapien
159	31	70.5	601	1	YFKS_SCHPO	P87132	schizosach	232	31	68.2	158	1	UBCT_HUMAN	O09181	mesocricetu
160	31	70.5	611	1	IF4B_HUMAN	P23588	homo sapien	233	31	68.2	158	1	UBCT_MESAU	P02810	homo sapien
161	31	70.5	656	1	DCHS_RAT	P16453	rattus norv	234	31	68.2	166	1	PRPC_HUMAN	Q8TCY5	homo sapien
162	31	70.5	658	1	Y285_HUMAN	O99144	sus scrofa	235	31	68.2	173	1	FALP_HUMAN	O9CG40	mus musculus
163	31	70.5	668	1	SG1_PIG	O95447	homo sapien	236	31	68.2	182	1	CXZI_MOUSE	P36054	saccharomyc
164	31	70.5	670	1	CUL3_HUMAN	P58332	sus scrofa	237	31	68.2	211	1	RCN1_YEAST	P10161	homo sapien
165	31	70.5	682	1	AMPH_CHICK	P58332	sus scrofa	238	31	68.2	234	1	PRPW_HUMAN	O53392	mycobacteri
166	31	70.5	682	1	AMPH_CHICK	O08838	rattus norv	239	31	68.2	243	1	YK42_MYCTU	P10163	homo sapien
167	31	70.5	687	1	WHIT_DROME	P10090	drosophila	240	31	68.2	247	1	PRB4_HUMAN	O05431	arabidopsis
168	31	70.5	695	1	AMPH_HUMAN	P49418	homo sapien	241	31	68.2	249	1	APX1_ARATH	P48534	pisum sativ
169	31	70.5	724	1	KN3_PIG	P58332	sus scrofa	242	31	68.2	251	1	PRP2_MOUSE	O18973	caenorhabd1
170	31	70.5	731	1	KN3_MOUSE	P70605	rattus norv	243	31	68.2	273	1	HMD1_CAEEL	P10162	homo sapien
171	31	70.5	732	1	KN3_RAT	Q9UP6	homo sapien	244	31	68.2	276	1	PRPL_HUMAN	O00165	homo sapien
172	31	70.5	733	1	SAB2_HUMAN	O8V14	mus musculus	245	31	68.2	279	1	HAXI_HUMAN	Q9B011	cercocebus
173	31	70.5	733	1	SAB2_MOUSE	O9UG16	homo sapien	246	31	68.2	280	1	TNFE_CERTO	O9MY16	macaca mula
174	31	70.5	736	1	KN3_HUMAN	O12797	homo sapien	247	31	68.2	280	1	TNFE_HUMAN	P48023	homo sapien
175	31	70.5	757	1	ASPH_HUMAN	P1257	porphyra pu	248	31	68.2	281	1	TNFE_HUMAN	P18174	canis fami1
176	31	70.5	763	1	IF2C_PORPU	P34595	caenorhabd1	249	31	68.2	285	1	INVO_CANFA	O81Z29	homo sapien
177	31	70.5	773	1	YOD3_CAEEL	P41002	homo sapien	250	31	68.2	292	1	FX16_HUMAN	P27021	human respi
178	31	70.5	786	1	CG2F_HUMAN	P38996	saccharomyc	251	31	68.2	297	1	VGIG_HRSV2		
179	31	70.5	802	1	NAB3_YEAST			252	31	68.2					

253	30	68.2	297	1	VGLG_HRSV3	P27022 human respi	326	30	68.2	443	1	RBL_VERBO	P36490 verbera bon
254	30	68.2	298	1	VGLG_HRSVA	P03423 human respi	327	30	68.2	443	1	RBL_VITCA	P05994 villareia c
255	30	68.2	299	1	VGKG_HRSVU	P20895 human respi	328	30	68.2	443	1	SOX3_HUMAN	P41325 homo sapien
256	30	68.2	309	1	SOX3_XENLA	P55863 xenopus lae	329	30	68.2	444	1	RBL_GINBI	P48704 ginkgo bilo
257	30	68.2	315	1	RPO4_THETH	Q929h6 theturus the	330	30	68.2	444	1	RBL_WELMT	P48719 welwitschia
258	30	68.2	318	1	MYOD_RAT	P02346 rattus norv	331	30	68.2	445	1	GD1B_HUMAN	P50395 homo sapien
259	30	68.2	323	1	GC_RABIT	P01870 corytolagus	332	30	68.2	445	1	RBL_CALDI	P36483 callitriche
260	30	68.2	327	1	Z444_HUMAN	Q8n0y2 homo sapien	333	30	68.2	446	1	RBL_EXAAF	P05989 exacum affi
261	30	68.2	331	1	PRP1_HUMAN	P04280 homo sapien	334	30	68.2	447	1	RBL_CAMLE	Q05694 canassia le
262	30	68.2	334	1	FX16_MOUSE	Q9qzms mus musculu	335	30	68.2	447	1	RBL_CONTR	Q05988 convolvulus
263	30	68.2	346	1	PF5E_ECOLI	P06128 escherichia	336	30	68.2	447	1	RBL_LIGUV	Q05991 ligustrum v
264	30	68.2	349	1	US30_HCMVA	P09706 human cytom	337	30	68.2	448	1	RBL_EUCLU	P28414 eucryphia l
265	30	68.2	375	1	SOX3_MOUSE	P01784 mus musculu	338	30	68.2	449	1	RBL_HIPRI	P31189 hippocratea
266	30	68.2	376	1	PEXE_MOUSE	Q9390 mus musculu	339	30	68.2	449	1	RBL_SALPL	P31202 saliccia pal
267	30	68.2	390	1	STAD_OLEEU	Q43593 olea europae	340	30	68.2	449	1	RBL_ZAMZA	Q06681 zantediaca
268	30	68.2	390	1	STAD_OKISA	Q40731 ozyra sativ	341	30	68.2	450	1	FOKE_CHLEN	Q92768 c foliae sy
269	30	68.2	394	1	RBL_ALIPL	P34767 allama plan	342	30	68.2	450	1	RBL_CRAMA	P28395 crassula ma
270	30	68.2	394	1	RBL_BARIO	Q05795 barclaya lo	343	30	68.2	450	1	RBL_SEDRU	P28455 sedum rubro
271	30	68.2	394	1	RBL_BRASC	Q05796 braesia sc	344	30	68.2	453	1	RBL_ASPIA	Q31809 asperula la
272	30	68.2	394	1	RBL_CABCA	Q05797 cabomba car	345	30	68.2	453	1	RBL_CRUAN	Q31846 crucianella
273	30	68.2	394	1	RBL_CERDE	Q05798 ceratophyll	346	30	68.2	453	1	RBL_CRUGL	Q31892 cruciata gl
274	30	68.2	394	1	RBL_EURPE	Q05799 eurypale fer	347	30	68.2	453	1	RBL_GALAL	Q32255 galium albu
275	30	68.2	394	1	RBL_NELLU	Q05800 nelumbo lut	348	30	68.2	453	1	RBL_GALAP	Q32256 galium apar
276	30	68.2	394	1	RBL_NUPVA	Q05801 nuphar vari	349	30	68.2	453	1	RBL_GALCO	Q32271 galium cors
277	30	68.2	394	1	RBL_NYMOD	Q05802 nympheae od	350	30	68.2	453	1	RBL_GALEL	Q32283 galium elon
278	30	68.2	394	1	RBL_VICCCZ	Q05803 victoria cr	351	30	68.2	453	1	RBL_GALLU	Q32303 galium lucu
279	30	68.2	396	1	STAD_HRIAN	Q06456 helianthus	352	30	68.2	453	1	RBL_GALPA	Q32345 galium patu
280	30	68.2	398	1	CIW4_MOUSE	Q08454 mus musculu	353	30	68.2	453	1	RBL_GALPR	Q32344 galium patl
281	30	68.2	399	1	STAS_BRANA	Q01771 braesia na	354	30	68.2	453	1	RBL_GALSC	Q32360 galium scab
282	30	68.2	403	1	YD50_PROMM	P59919 prochloroco	355	30	68.2	453	1	RBL_HYDFO	Q32397 hydrophytum
283	30	68.2	404	1	KVB3_RAT	Q63494 rattus norv	356	30	68.2	453	1	RBL_PHOST	Q32808 phopsis sty
284	30	68.2	406	1	RBL_GREBI	P43329 crepidomane	357	30	68.2	453	1	RBL_RUBTI	Q33050 rubia tinct
285	30	68.2	410	1	RBL_GUEJA	P48705 gleichenia	358	30	68.2	453	1	RBL_SHEAR	Q33062 sherardia a
286	30	68.2	411	1	STAD_SOYBN	Q42807 glycine max	359	30	68.2	453	1	RBL_VALMU	Q33574 valentia ma
287	30	68.2	411	1	VG66_HSV11	Q00154 ictaluriid h	360	30	68.2	455	1	RBL_ACAFA	P93398 acacia farn
288	30	68.2	414	1	SX17_HUMAN	Q9h612 homo sapien	361	30	68.2	455	1	RBL_BROCO	P93388 brownia coc
289	30	68.2	416	1	RBL_CHEBI	P43227 cheitropleur	362	30	68.2	455	1	RBL_CASDI	P93680 caesia didy
290	30	68.2	416	1	RBL_SPTMR	P36488 spigelia ma	363	30	68.2	455	1	RBL_BRYCG	Q33438 erythrina c
291	30	68.2	419	1	SX17_MOUSE	Q61473 mus musculu	364	30	68.2	455	1	RBL_LUPRA	P92398 lupinus acil
292	30	68.2	420	1	RBL_ANEME	Q31674 anemula mexi	365	30	68.2	455	1	RBL_LUPAB	P52781 lupinus alb
293	30	68.2	426	1	RBL_HORVU	P05698 hordium vul	366	30	68.2	455	1	RBL_LUPAE	P92397 lupinus alb
294	30	68.2	427	1	TR16_HUMAN	Q90813 homo sapien	367	30	68.2	455	1	RBL_LUPAL	P92396 lupinus alb
295	30	68.2	430	1	SYTB_MOUSE	Q90n03 mus musculu	368	30	68.2	455	1	RBL_LUPAN	P52775 lupinus pol
296	30	68.2	430	1	SYTB_RAT	Q08835 rattus norv	369	30	68.2	455	1	RBL_LUPCO	P92400 lupinus cos
297	30	68.2	435	1	RBL_DROBR	P28404 drosera bur	370	30	68.2	455	1	RBL_LUPDE	P92401 lupinus den
298	30	68.2	436	1	RBL_BRYLI	P28386 byblis linl	371	30	68.2	455	1	RBL_LUPMT	P92406 lupinus mic
299	30	68.2	436	1	RBL_SANCA	P28450 sanguinaria	372	30	68.2	455	1	RBL_LUPNA	P92407 lupinus nan
300	30	68.2	440	1	RBL_BAMGL	P51594 bambusa gla	373	30	68.2	455	1	RBL_LUPPO	P52775 lupinus pol
301	30	68.2	440	1	RBL_DICAN	P48701 dicksonia a	374	30	68.2	455	1	RBL_TAMIN	P93689 tamariindus
302	30	68.2	440	1	RBL_PTYGA	Q08360 ptychomitri	375	30	68.2	457	1	RBL_PHECO	P31197 phelline co
303	30	68.2	441	1	RBL_APOCA	Q05984 apocynum ca	376	30	68.2	459	1	RBL_APRGR	P28380 apium grave
304	30	68.2	441	1	RBL_ASCCX	P36480 asclepias e	377	30	68.2	459	1	RBL_CEPFO	P28390 cephalotus
305	30	68.2	441	1	RBL_BEGMS	P28383 begonia met	378	30	68.2	459	1	RBL_CBRGU	P28391 ceratopetal
306	30	68.2	441	1	RBL_CORSA	Q05579 coriandrum	379	30	68.2	459	1	RBL_CORLA	P31183 corynocarpu
307	30	68.2	441	1	RBL_DARCA	P28398 darlingtoni	380	30	68.2	459	1	RBL_GAREL	P28416 garveya elii
308	30	68.2	441	1	RBL_DRODC	P28406 drosera dic	381	30	68.2	459	1	RBL_GRUCH	P28418 geum chiloe
309	30	68.2	441	1	RBL_DROPT	P28410 drosera pec	382	30	68.2	459	1	RBL_HRUMI	P28423 heuchera mi
310	30	68.2	441	1	RBL_FOUPP	Q05590 fouquieria	383	30	68.2	459	1	RBL_MORAL	P28431 morus alba
311	30	68.2	441	1	RBL_GLYEC	Q62970 glycyrrhiza	384	30	68.2	459	1	RBL_NYPRF	P28431 nyssa frutic
312	30	68.2	441	1	RBL_HELNU	P28422 hellamphora	385	30	68.2	459	1	RBL_NYSOG	P28435 nyssa ogech
313	30	68.2	441	1	RBL_POLRE	Q05992 polemonium	386	30	68.2	459	1	RBL_PAREI	P28437 parassia f
314	30	68.2	441	1	RBL_SYMAL	Q05993 symphoricar	387	30	68.2	459	1	RBL_PRUPO	P28445 prunus dome
315	30	68.2	441	1	RBL_VIOSO	Q05995 viola sorar	388	30	68.2	459	1	RBL_BORGO	P28448 boridula go
316	30	68.2	443	1	RBL_ABIFI	Q78288 abies firma	389	30	68.2	459	1	RBL_SAXIN	P28452 saxifraga l
317	30	68.2	443	1	RBL_ABIRH	Q78259 abies homol	390	30	68.2	459	1	RBL_STRLC	P43600 streptopus
318	30	68.2	443	1	RBL_ABIMR	Q78261 abies marie	391	30	68.2	460	1	RBL_CRYJA	P48696 cryptomeria
319	30	68.2	443	1	RBL_ABISA	Q78262 abies sach	392	30	68.2	460	1	RBL_CUNTA	Q32026 cunninghami
320	30	68.2	443	1	RBL_ABIVE	Q78260 abies veitc	393	30	68.2	460	1	RBL_HALCL	Q09890 halestia car
321	30	68.2	443	1	RBL_ANTMA	Q05554 antirrhinum	394	30	68.2	463	1	RBL_GERGR	P28417 geranium gr
322	30	68.2	443	1	RBL_BOROF	Q05985 borago ofit	395	30	68.2	463	1	RBL_PELHO	P28439 pelargonium
323	30	68.2	443	1	RBL_BUDDA	P36482 buddleja da	396	30	68.2	465	1	RBL_ACESA	P28376 acer saccha
324	30	68.2	443	1	RBL_CAHBE	Q05986 callitriche	397	30	68.2	465	1	RBL_ACTCH	P28377 actinidia c
325	30	68.2	443	1	RBL_SESIN	P36487 sesamum ind	398	30	68.2	465	1	RBL_ALIAL	Q07209 atlantus a

399	30	68.2	465	1	RBL_BAURU	Q31730	bauera rubi
400	30	68.2	465	1	RBL_BURIN	P28385	bursera ina
401	30	68.2	465	1	RBL_BYRCR	P28387	byrsocoma c
402	30	68.2	465	1	RBL_CASFS	O20304	casaria fist
403	30	68.2	465	1	RBL_CASLI	P28389	casarina l
404	30	68.2	465	1	RBL_CLITE	O20346	clitoria te
405	30	68.2	465	1	RBL_CORCA	P28393	cornus cana
406	30	68.2	465	1	RBL_CORFO	O31983	cornus flor
407	30	68.2	465	1	RBL_COROB	O32040	cornus obl
408	30	68.2	465	1	RBL_COROF	O32042	cornus offi
409	30	68.2	465	1	RBL_COROT	O32041	cornus oblo
410	30	68.2	465	1	RBL_CYRRA	P28396	cyrilla rac
411	30	68.2	465	1	RBL_DABSP	P28397	daphniphyll
412	30	68.2	465	1	RBL_DILIN	P28400	dillenia in
413	30	68.2	465	1	RBL_EPASP	P28432	epacis sp.
414	30	68.2	465	1	RBL_EPHTW	O32223	ephedra twe
415	30	68.2	465	1	RBL_EUCUL	P28415	eucornia ul
416	30	68.2	465	1	RBL_FRANR	P48703	fragaria an
417	30	68.2	465	1	RBL_HAMMO	P28419	hamamelis m
418	30	68.2	465	1	RBL_HUMMA	P28424	humilia bal
419	30	68.2	465	1	RBL_IDEFO	O9XP5	idesia poly
420	30	68.2	465	1	RBL_ILECR	P28446	ilex crenat
421	30	68.2	465	1	RBL_MANZA	P28430	manilkara z
422	30	68.2	465	1	RBL_MORRU	O32635	morus rubra
423	30	68.2	465	1	RBL_MYRCE	P28442	myrica ceri
424	30	68.2	465	1	RBL_NEPAL	P28443	nepenthes a
425	30	68.2	465	1	RBL_PLAOC	P28441	platanus oc
426	30	68.2	465	1	RBL_PLAVR	P28442	platytheca
427	30	68.2	465	1	RBL_POLCR	P28443	polygala cr
428	30	68.2	465	1	RBL_QUIIN	P28446	quisqualis
429	30	68.2	465	1	RBL_RHOHI	P28447	rhododendro
430	30	68.2	465	1	RBL_SARPL	P28451	sarracenia
431	30	68.2	465	1	RBL_TROAR	P28458	trochodendr
432	30	68.2	465	1	RBL_ULMAL	O33245	ulmus alata
433	30	68.2	465	1	RSP4_CHLRE	O01656	chlamydomon
434	30	68.2	466	1	RBL_ADOBO	O93000	adentum obe
435	30	68.2	466	1	RBL_ADOBO	P28378	adoxa mosch
436	30	68.2	466	1	RBL_AESPA	O31827	aeschulus pa
437	30	68.2	466	1	RBL_APHSI	P28379	asaphandra
438	30	68.2	466	1	RBL_ASACA	P28479	asarum cana
439	30	68.2	466	1	RBL_AVECA	O9m747	averrhoa ca
440	30	68.2	466	1	RBL_BARRR	P28382	barleria pr
441	30	68.2	466	1	RBL_BEAGR	O99001	beaumontia
442	30	68.2	466	1	RBL_BERLA	P36481	berzelia la
443	30	68.2	466	1	RBL_BETNI	P28384	betula nigra
444	30	68.2	466	1	RBL_BIXOR	O19872	bixa orella
445	30	68.2	466	1	RBL_BUTAR	O19989	butleria ar
446	30	68.2	466	1	RBL_CALFL	P28388	caltha palu
447	30	68.2	466	1	RBL_CERJA	O05987	ceratidiphyll
448	30	68.2	466	1	RBL_CORNO	O33369	cornus kous
449	30	68.2	466	1	RBL_CORYV	P28394	cortaria my
450	30	68.2	466	1	RBL_CUCPE	P28637	cucubita p
451	30	68.2	466	1	RBL_DICOMU	P28401	dionea mus
452	30	68.2	466	1	RBL_DRIMI	P28402	drims wint
453	30	68.2	466	1	RBL_DROBI	P28403	drosera bin
454	30	68.2	466	1	RBL_DROCA	P28405	drosera cap
455	30	68.2	466	1	RBL_DROFI	P28407	drosera fil
456	30	68.2	466	1	RBL_DROUJ	P28408	drosophyllu
457	30	68.2	466	1	RBL_DRORE	P28411	drosera reg
458	30	68.2	466	1	RBL_EREMA	O33443	eremochamu
459	30	68.2	466	1	RBL_HARGR	P28420	harpagophyt
460	30	68.2	466	1	RBL_HEDHE	P28421	hedera hell
461	30	68.2	466	1	RBL_JUSOD	P28428	justicia od
462	30	68.2	466	1	RBL_LOBSP	P28429	lobelia sp.
463	30	68.2	466	1	RBL_MOROL	P48708	moringa ole
464	30	68.2	466	1	RBL_MANDU	O20241	mandina dom
465	30	68.2	466	1	RBL_NELCA	P28433	nelsonia ca
466	30	68.2	466	1	RBL_OXADI	P28436	oxalis dill
467	30	68.2	466	1	RBL_PINCA	P28440	pinguicula
468	30	68.2	466	1	RBL_POLSI	O9gh8	poliothyrsi
469	30	68.2	466	1	RBL_PROUJ	P28444	proscodaea
470	30	68.2	466	1	RBL_RUTR	P28449	rutylia frut
471	30	68.2	466	1	RBL_SAUCE	P36486	saururus ce

472	30	68.2	466	1	RBL_SITGA	P25837	silene gall
473	30	68.2	466	1	RBL_THERPO	P28457	theopetia p
474	30	68.2	466	1	RBL_VITAE	P28460	vitis aesti
475	30	68.2	467	1	RBL_CALUS	P25829	calamus usi
476	30	68.2	467	1	RBL_CEDAT	O9ggx6	cedrus atla
477	30	68.2	467	1	RBL_ERICA	P28413	eridictyon
478	30	68.2	467	1	RBL_HYDVI	P28425	hydrorhizulu
479	30	68.2	467	1	RBL_JASUS	P28427	jasminum su
480	30	68.2	467	1	RBL_PHOKE	P28462	phoenix rec
481	30	68.2	467	1	RBL_SCUBO	P28453	scutellaria
482	30	68.2	467	1	RBL_SERRE	P25836	serenoa rep
483	30	68.2	467	1	RBL_TASIN	P28456	tasmanian i
484	30	68.2	468	1	RBL_ANTIHE	O31659	anthospermum
485	30	68.2	468	1	RBL_ANTIUS	O31659	anthocercis
486	30	68.2	468	1	RBL_CAPBA	O31651	capiscum ba
487	30	68.2	468	1	RBL_CATSP	O33383	catesbaea s
488	30	68.2	468	1	RBL_CORAT	O31348	cornus alie
489	30	68.2	468	1	RBL_CONGU	O98883	conouputa
490	30	68.2	468	1	RBL_DATST	P48698	datuna etra
491	30	68.2	468	1	RBL_NOLSP	O32659	nolana spat
492	30	68.2	468	1	RBL_PANUS	O98668	pandorea ja
493	30	68.2	468	1	RBL_SALDI	P36485	salvia divi
494	30	68.2	468	1	RBL_SOLGR	O33101	solandra gr
495	30	68.2	468	1	RBL_TECST	O98671	tecma stan
496	30	68.2	469	1	RBL_AKABI	O07821	akania bidw
497	30	68.2	469	1	RBL_ANTIUV	O31672	atriplex lu
498	30	68.2	469	1	RBL_ATRAP	P19160	atriplex pa
499	30	68.2	469	1	RBL_BREMA	O31738	brexia mada
500	30	68.2	469	1	RBL_CALCA	O31750	calycophyll

ALIGNMENTS

RESULT 1

ID	UROC_HUMAN	STANDARD,	PRT,	431 AA.
AC	P00749; Q15844; Q16618; Q969W6;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	20-MAR-1987 (Rel. 04, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (UPA)			
DE	(U-plasminogen activator).			
GN	PLAU.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=65215647; PubMed=2987867;			
RA	Riccio A., Grimaldi G., Verde P., Sebastio G., Boast S., Blas F.;			
RT	"The human urokinase-plasminogen activator gene and its promoter.";			
RT	Nucleic Acids Res. 13:2759-2771(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Holmes W.E., Pennica D., Blaber M., Ray M.W., Guenzler W.A.,			
RT	Steffens G.J., Heyneker H.L.;			
RT	"Cloning and expression of the gene for pro-urokinase in Escherichia			
RT	coli.";			
RT	Biotechnology 3:923-929(1985).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=6056954; PubMed=2415429;			
RA	Nagai M., Hiramatsu R., Kaneda T., Hayasuke N., Arimura H.,			
RT	Nishida M., Suyama T.;			
RT	"Molecular cloning of cDNA coding for human prepro-urokinase.";			
RT	Gene 36:183-188(1985).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85203359; PubMed=3888571;			
RA	Jacobs P., Cravador A., Lorian R., Brockly F., Colau B., Chuchana P.,			
RA	van Eise A., Herzog A., Bollen A.;			

RT "Molecular cloning, sequencing, and expression in *Escherichia coli* of
RT human preprourokinase cDNA." ;
RT DNA 4:139-146(1985).
RN [5]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Peel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muny D.M., Sodegren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smilins D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences." ;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 66-431 FROM N.A.
RX MEDLINE=84272706; PubMed=6589620;
RT Verde P., Stoppelli M.P., Galeffi P., di Nocera P., Blasi F.;
RT "Identification and primary sequence of an unspliced human urokinase
RT poly(A) + RNA." ;
RL Proc. Natl. Acad. Sci. U.S.A. 81:4727-4731(1984).
RN [8]
RP SEQUENCE OF 21-177.
RX MEDLINE=83055084; PubMed=6754569;
RA Gunzler W.A., Steffens G.J., Otting F., Kim S.-M.A., Frankus E.,
RA Flohe L.;
RT "The primary structure of high molecular mass urokinase from human
RT urine. The complete amino acid sequence of the A chain." ;
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1155-1165(1982).
RN [9]
RP SEQUENCE OF 156-176 AND 179-224.
RX MEDLINE=83003608; PubMed=6749491;
RA Schaller U., Nick H., Rickli E.B., Gillesen D., Lergier W.,
RA Studer R.O.;
RT "Human low-molecular-weight urinary urokinase. Partial
RT characterization and preliminary sequence data of the two polypeptide
RT chains." ;
RL Eur. J. Biochem. 125:251-257(1982).
RN [10]
RP SEQUENCE OF 158-410.
RX MEDLINE=83055099; PubMed=6754572;
RA Steffens G.J., Gunzler W.A., Otting F., Frankus E., Flohe L.;
RT "The complete amino acid sequence of low molecular mass urokinase
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RL Hoppe-Seyler's Z. Physiol. Chem. 363:1043-1058(1982).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=96000858; PubMed=8591045;
RA Sprengon G., Phillips C., Nowak U.K., Ponting C.P., Saunders D.,
RA Dobson C.M., Stuart D.I., Jones E.Y.;
RT "The crystal structure of the catalytic domain of human
RT urokinase-type plasminogen activator." ;
RL Structure 3:681-691(1995).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 159-411.
RX MEDLINE=20266327; PubMed=10805774;
RA Speit S., Jacob U., Arroyo de Prada N., Sturzebecher J., Wilhelm O.G.,
RA Bode W., Magdolen V., Huber R., Moroder L.;
RT "4-(4-aminomethyl)phenylguanidine derivatives as nonpeptidic highly
RT selective inhibitors of human urokinase." ;
RL Proc. Natl. Acad. Sci. U.S.A. 97:5113-5118(2000).
RN [13]
RP STRUCTURE BY NMR.
RX MEDLINE=89127526; PubMed=2536903;
RA Oswald R.E., Bogusky M.J., Bamberger M., Smith R.A.G., Dobson C.M.;
RT "Dynamics of the multidomain fibrinolytic protein urokinase from two-
RT dimensional NMR." ;
RL Nature 337:579-582(1989).
RN [14]
RP STRUCTURE BY NMR OF 67-155.
RX MEDLINE=93003110; PubMed=1327118;
RA Li X., Smith R.A.G., Dobson C.M.;
RT "Sequential 1H NMR assignments and secondary structure of the kringle
RL domain from urokinase." ;
RN Biochemistry 31:9562-9571(1992).
RN [15]
RP STRUCTURE BY NMR OF 67-155.
RX MEDLINE=94149701; PubMed=8107091;
RA Li X., Bokman A.M., Llinas M., Smith R.A.G., Dobson C.M.;
RT "Solution structure of the kringle domain from urokinase-type
RT plasminogen activator." ;
RL J. Mol. Biol. 235:1548-1559(1994).
RN [16]
RP VARIANT LEU-141.
RX MEDLINE=96186279; PubMed=8652631;
RA Yoshimizu M., Ushiyama Y., Sakai M., Tamaki S., Hara H., Takahashi K.,
RA Sawasaki Y., Hanada K.;
RT "Characterization of single chain urokinase-type plasminogen
RT activator with a novel amino-acid substitution in the kringle
RT structure." ;
RL Biochim. Biophys. Acta 1293:83-89(1996).
RN [17]
RP VARIANT LEU-141.
RX MEDLINE=97218551; PubMed=9065988;
RA Come B., Berczy M., Belin D.;
RT "Detection of polymorphisms in the human urokinase-type plasminogen
RT activator gene." ;
RL Thromb. Haemost. 77:434-435(1997).
RN [18]
RP ERRATUM.
RA Come B., Berczy M., Belin D.;
RL Thromb. Haemost. 78:973-973(1997).
RN [19]
RP VARIANT LEU-141.
RX MEDLINE=97337920; PubMed=9194591;
RA Turkmen B., Schmitt M., Schmalzfeldt B., Trommler P., Hell W.,
RA Creutzburg S., Graeff H., Magdolen V.;
RT "Mutational analysis of the genes encoding urokinase-type plasminogen
RT activator (uPA) and its inhibitor PAI-1 in advanced ovarian cancer." ;
RL Electrophoresis 18:686-689(1997).
CC -1- FUNCTION: Potent plasminogen activator and is clinically used for
CC therapy of thrombolytic disorders.
CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
CC plasminogen to form plasmin.
CC -1- SUBUNIT: Found in high and low molecular mass forms. Each consists
CC of two chains, A and B. The high molecular mass form contains a
CC long chain A. Cleavage occurs after residue 155 in the low
CC molecular mass form to yield a short A1 chain.
CC -1- PHARMACEUTICAL: Available under the name Abbockinase (Abbott). Used
CC in Pulmonary Embolism (PE) to initiate fibrinolysis.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -----
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DR EMBL; X02419; CAA26268.1; -
DR EMBL; M15476; AAA61253.1; -
DR EMBL; D00244; BAA00175.1; -
DR EMBL; D11143; BAA01919.1; -
DR EMBL; X02760; CAA26535.1; -
DR EMBL; AF377330; AAK53822.1; -
DR EMBL; BC013575; AAH13575.1; -
DR EMBL; K03226; AAC97138.1; -
DR EMBL; K02286; AAA61252.1; -
DR EMBL; A21571; CAA01590.1; -
DR EMBL; A18397; CAA01390.1; -
DR PIR; A00931; UKHU.
DR PDB; 1KDU; 31-OCT-93.

Query Match      100.0%; Score 44; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KPSSPPEE 8
Db      156 KPSSPPEE 163

RESULT 2
UROK_PAPCV
ID UROK_PAPCV STANDARD; PRT; 433 AA.
AC P16227;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urokinase-type plasminogen activator precursor (RC 3.4.21.73) (uPA)
DE (U-plasminogen activator).
GN PLAU.
OS Papio cynocephalus (Yellow baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoinae; Papio.
OX NCBI_TaxID=9556;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thoracic aorta;
RX MEDLINE=90287734; PubMed=2113276;
RA Au Y.P.T., Wang T.W., Clowes A.W.;
RT "Nucleotide and deduced amino acid sequences of baboon urokinase-type
RT plasminogen activator."
RL Nucleic Acids Res. 18:3411-3411(1990).
CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
CC plasminogen to form plasmin.
CC -1- SUBUNIT: Found in high and low molecular mass forms. Each consists
CC of two chains, A and B. The high molecular mass form contains a
CC long chain A. Cleavage occurs after residue 155 in the low
CC molecular mass form to yield a short A1 chain (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL; X51935; CAA36200.1; -
DR PIR; S14687; UKBAY.
DR HSSP; P00749; ILMW.
DR MEROPS; S01.231; -
DR InterPro; IPR009003; Cys_Ser_tryptsin.

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DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR006001; Kringle.
DR InterPro; IPR008293; Pept_S1a uPA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00051; Kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PIRSF; PIRSF001144; Uro_plasm_act; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PSS0026; EGF_3; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PSS0070; KRINGLE_2; 1.
DR PROSITE; PSS0240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR plasminogen activation; Hydrolyase; Serine protease; Glycoprotein;
KW Kringle; EGF-like domain; Zymogen; Signal.
FT SIGNAL 1 20
FT CHAIN 21 433 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
FT CHAIN 21 176 CHAIN A (BY SIMILARITY).
FT CHAIN 155 176 SHORT A CHAIN (A1) (BY SIMILARITY).
FT CHAIN 178 433 CHAIN B (BY SIMILARITY).
FT DOMAIN 26 62 EGF-LIKE.
FT DOMAIN 69 150 KRINGLE.
FT DOMAIN 151 177 CONNECTING PEPTIDE.
FT DOMAIN 178 433 SERINE PROTEASE.
FT DISUFID 30 38 BY SIMILARITY.
FT DISUFID 32 50 BY SIMILARITY.
FT DISUFID 52 50 BY SIMILARITY.
FT DISUFID 52 61 BY SIMILARITY.
FT DISUFID 167 298 INTERCHAIN (BY SIMILARITY).
FT DISUFID 208 224 BY SIMILARITY.
FT DISUFID 216 287 BY SIMILARITY.
FT DISUFID 315 384 BY SIMILARITY.
FT DISUFID 347 363 BY SIMILARITY.
FT DISUFID 374 402 BY SIMILARITY.
FT ACT_SITE 223 223 CHARGE RELAY SYSTEM.
FT ACT_SITE 274 274 CHARGE RELAY SYSTEM.
FT ACT_SITE 378 378 CHARGE RELAY SYSTEM.
FT CARBOHYD 324 324 N-LINKED (GLCNAC...) (BY SIMILARITY).
SQ SEQUENCE 433 AA; 48595 MW; 816D22DFEDC8792 CRC64;

Query Match      100.0%; Score 44; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KPSSPPEE 8
Db      155 KPSSPPEE 162

RESULT 3
PEDF_HUMAN
ID PEFH_HUMAN STANDARD; PRT; 418 AA.
AC P36955; Q96CT1; Q96R01; Q9BMA4;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pigment epithelium-derived factor precursor (PEDF) (EPC-1).
GN SERPINF1 OR PEDF.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

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FT TURN 146 147
 FT HELIX 152 162
 FT STRAND 167 168
 FT HELIX 173 187
 FT TURN 188 190
 FT STRAND 205 214
 FT STRAND 217 219
 FT HELIX 223 225
 FT STRAND 227 232
 FT STRAND 238 256
 FT TURN 257 260
 FT STRAND 261 268
 FT TURN 269 271
 FT STRAND 272 279
 FT HELIX 287 290
 FT TURN 291 292
 FT HELIX 295 304
 FT STRAND 306 315
 FT STRAND 317 324
 FT HELIX 326 330
 FT TURN 331 335
 FT HELIX 336 339
 FT TURN 344 346
 FT STRAND 353 364
 FT STRAND 368 370
 FT STRAND 387 389
 FT STRAND 394 400
 FT TURN 401 403
 FT STRAND 406 412
 FT TURN 415 416
 SQ SEQUENCE 418 AA, 46342 MW, 298573A62EA51B85 CRC64;

Query Match
 Best Local Similarity 81.8%; Score 36; DB 1; Length 418;
 Pred. No. 72;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 PSSPPE 8
 Db 22 PASPPE 28

RESULT 4
 YB96_HUMAN STANDARD; PRT; 892 AA.
 AC Q96KM6; Q9ULM4; Rel. 41, Created
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical zinc finger protein KIAA1196.
 GN KIAA1196.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; Pubmed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Savvides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.W., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Cowile G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehesvalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McComachie L.J., McIay K., McMuray A.A.,
 RA Milne S.A., Mistry D., Moore M.U.F., Mullikin J.C., Nickerson T.,

RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prachalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sultson J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [2]
 RP SEQUENCE OF 42-892 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20039619; Pubmed=10574462;
 RA Nagase T., Ishikawa K.-I., Kikuno R., Hirosewa M., Nomura N.,
 RA Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 6:337-345(1999).
 RN [3]
 RP SEQUENCE OF 425-892 FROM N.A.
 RC TISSUE=Testis;
 RA Duesterhoeft A., Lauber J., Mewes H.-W., Weil B., Wiemann S.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: May function as a transcription factor.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.

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 CC -----
 DR EMBL; AL118506; CAC15498.3; -;
 DR EMBL; AB033022; BAA86510.1; -;
 DR EMBL; AL834525; CAD39181.1; -;
 DR InterPro; IPR007087; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 5.
 DR SMART; SM00355; ZNF_C2H2; 6.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
 KW Hypothetical protein; Transcription regulation; DNA-binding;
 KW Metal-binding; Zinc-finger; Nuclear protein; Repeat.
 FT ZN_FING 105 129 C2H2-TYPE (ATYPICAL).
 FT ZN_FING 140 163 C2H2-TYPE.
 FT ZN_FING 540 563 C2H2-TYPE.
 FT ZN_FING 594 618 C2H2-TYPE (ATYPICAL).
 FT ZN_FING 630 653 C2H2-TYPE (ATYPICAL).
 FT ZN_FING 750 774 C2H2-TYPE (ATYPICAL).
 FT ZN_FING 784 807 C2H2-TYPE.
 SQ SEQUENCE 892 AA; 97264 MW; 50449CA476DFCE4DF CRC64;

Query Match
 Best Local Similarity 81.8%; Score 36; DB 1; Length 892;
 Pred. No. 1,6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 2 PSSPPE 8
 Db 407 PASPPE 413

RESULT 5
 PIGO_HUMAN STANDARD; PRT; 1088 AA.
 AC Q8TEQ8; Q8TDS8; Q96CS9; Q9BVN9; Q9Y4B0;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

15-MAR-2004 (Rel. 43, last annotation update)
 Phosphatidylinositol-glycan biosynthesis, class O protein (PIG-O).
 Homo sapiens (Human).
 CC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Testis;
 RA Ansoigne W., Winkler U., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RN Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Spleen;
 RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;
 RN "The nucleotide sequence of a long cDNA clone isolated from human
 spleen";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Lameudin J.E., McCready P.M., Skowronski E., Adamson A.W.,
 RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Scilwagen S.,
 RA Phan H., Velasco N., Ganes J., Dangman L., Poundstone P.,
 RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,
 RA Tranheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
 RA Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,
 RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
 RA Carraro A.V.;
 RN "Sequence analysis of a human PI clone containing the XRCC9 DNA repair
 gene";
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Ductenium;
 RA MEDLINE=2388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schlier G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Millaby S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gnaratine P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smilins D.E.,
 RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.;
 RN "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 601-968 FROM N.A.
 RA Takeda S., Kadowaki S., Haga T., Takeasu H., Mitaku S.;
 RN "Identification of G protein-coupled receptor genes from the human
 genome sequence";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Involved in GPI-anchor biosynthesis but not essential
 for this process. Involved, together with PIGF, in the transfer of
 ethanolamine phosphate to the third mannose of GPI (By
 similarity).
 CC -1- PATHWAY: GPI-anchor biosynthesis.
 CC -1- SUBUNIT: Forms a complex with PIGF. PIGF is required to stabilize
 PIGO (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 reticulum (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=Q8TRQ8-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q8TRQ8-2; Sequence=VSP_003944;
 CC Note=No experimental confirmation available;
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
 frameshift in position 46.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to
 frameshifts.
 CC -----
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 CC -----
 DR EMBL: AL833956; CAD38806.1; ALT_FRAME.
 DR EMBL: AK074064; BAB84890.1; ALT_FRAME.
 DR EMBL: AK090433; BAC03414.1; ALT_FRAME.
 DR EMBL: AC004472; AAC07985.1; ALT_SEQ.
 DR EMBL: BC029271; AAH29271.1; -.
 DR EMBL: BC001030; AAH01030.1; ALT_INIT.
 DR EMBL: BC013987; AAH13987.1; ALT_INIT.
 DR EMBL: AB083625; BAB89338.1; -.
 DR Genew; HGNC:23215; PIGO.
 DR GO; GO:0005789; C:endoplasmic reticulum membrane; ISS.
 DR GO; GO:0006506; P:GPI anchor biosynthesis; ISS.
 DR InterPro; IPR002591; Phosphodiect.
 DR Pfam; PF01663; Phosphodiect; 1.
 KW GPI-anchor biosynthesis; Transmembrane; Endoplasmic reticulum;
 KW Alternative splicing.
 FT TRANSMEM 4 24
 FT TRANSMEM 456 476 POTENTIAL.
 FT TRANSMEM 481 501 POTENTIAL.
 FT TRANSMEM 509 529 POTENTIAL.
 FT TRANSMEM 540 560 POTENTIAL.
 FT TRANSMEM 574 594 POTENTIAL.
 FT TRANSMEM 667 687 POTENTIAL.
 FT TRANSMEM 700 720 POTENTIAL.
 FT TRANSMEM 746 766 POTENTIAL.
 FT TRANSMEM 829 849 POTENTIAL.
 FT TRANSMEM 856 876 POTENTIAL.
 FT TRANSMEM 943 963 POTENTIAL.
 FT TRANSMEM 1013 1033 POTENTIAL.
 FT TRANSMEM 1047 1067 POTENTIAL.
 FT VARSPLIC 448 864 Missing (in isoform 2).
 FT FT 179 181 DIT -> ARG (IN REF. 4; AAH13987).
 FT CONFLICT 225 231 DVIAIAF -> EVSNQHV (IN REF. 4; AAH01030).
 FT CONFLICT 350 350 G -> Y (IN REF. 4; AAH29271).
 FT CONFLICT 353 353 D -> Y (IN REF. 4; AAH29271).
 FT CONFLICT 415 415 R -> KG (IN REF. 4).
 FT CONFLICT 883 968 PFTVQWASAVAMATQFVSGHQDPVPAIIMHAAPVGF
 FT PEGHSGCTWLPALVACANTPASHILPRAVGCPLILMPFCE
 FT SQGL -> KYLSDSIKNSDVASAPVFEVILLPLFLSLT
 FT EGMPHTTRKVFVLSILPAIAKQIDPSCWFPQFMERRDKS
 FT SSTKPCGNAASS (IN REF. 5).
 FT SQT
 SQ SEQUENCE 1088 AA; 118669 MW; 065985AC16D1D340 CRC64;
 Query Match 81.8%; Score 36; DB 1; Length 1088;
 Best Local Similarity 85.7%; Pred. No. 2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 PSSPPER 8
 Db 308 PSTPPER 314
 RESULT 6
 SIRA_YEAST

ID SIR4_YEAST STANDARD; PRT; 1358 AA.
AC P11978;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, last sequence update)
DT 28-FEB-2003 (Rel. 41, last annotation update)
DE Regulatory protein SIR4 (silent information regulator 4).
GN SIR4 OR STS OR ASD1 OR UTH2 OR YDR227W OR YD934.12.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88142836; PubMed=3325825;
RA Marshall M., Mahoney D., Rose A., Hicks J.B., Broach J.R.;
RT "Functional domains of SIR4, a gene required for position effect
RT regulation in Saccharomyces cerevisiae.";
RL Mol. Cell. Biol. 7:4441-4452(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95192063; PubMed=7885847;
RA Davies C.J., Hutchison C.A. III;
RT "Insertion site specificity of the transposon Tn3.";
RL Nucleic Acids Res. 23:507-514(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=S288c / AB972;
RA Murphy L., Harris D., Barrell B.G., Rajandream M.A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP REVIEW.
RX MEDLINE=21579783; PubMed=11722841;
RA Gasser S.M., Cockell M.M.;
RT "The molecular biology of the SIR proteins.";
RL Gene 279:1-16(2001).
CC -1- FUNCTION: The proteins SIR1 through SIR4 are required for
CC transcriptional repression of the silent mating type loci, HML and
CC HMR. The proteins SIR2 through SIR4 repress multiple loci by
CC modulating chromatin structure. Involves the compaction of
CC chromatin fiber into a more condensed form.
CC -1- SUBUNIT: Homodimer and interacts with SIR1, SIR2, SIR3 and RAPI C-
CC terminus.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -----
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CC -----
CC EMBL; M37249; AAA20881.1; -;
DR EMBL; U13239; AAC3144.1; -;
DR EMBL; Z48612; CA88507.1; -;
DR PIR; A29360; A29360.
DR GerMOnline; 140719; -;
DR SGD; S0002635; SIR4.
DR GO; GO:0000783; C:nuclear telomere cap complex; IDA.
DR GO; GO:0005724; C:nuclear telomeric heterochromatin; IDA.
DR GO; GO:0006303; P:double-strand break repair via nonhomologous...; IDA.
KW Transcription regulation; Repressor; DNA-binding; Nuclear protein;
KW Coiled coil.
FT DOMAIN 1277 1347 COILED COIL (POTENTIAL).
FT VARIANT 994 994 P -> L.
SQ SEQUENCE 1358 AA; 152061 MW; 96C698765964F094E CRC64;
Query Match 81.8%; Score 36; DB 1; Length 1358;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSSPPE 7
|||||:

Db 1131 KPSSPPD 1137
RESULT 7
CA1B_HUMAN STANDARD; PRT; 1806 AA.
AC P12107; Q14034; Q9UIT4; Q9UIT5; Q9UIT6;
DT 01-OCT-1989 (Rel. 12, Created)
DT 28-FEB-2003 (Rel. 41, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Collagen alpha 1(XI) chain precursor.
GN COL11A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90202924; PubMed=1690726;
RA Yoshida H., Ramirez F.;
RT "Pro-alpha 1(XI) collagen. Structure of the amino-terminal propeptide
RT and expression of the gene in tumor cell lines.";
RL J. Biol. Chem. 265:6423-6426(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS A, B AND C), AND VARIANTS STL2/MARSHALL
RP SYNDROME ARG-676; 921-GLN--PRO-926 DEL; 1313-PHE--GLY-1315 DEL AND
RP VAL-1516.
RX MEDLINE=20455728; PubMed=1046316;
RA Annunen S., Koerkoe J., Czarny M., Warman M.L., Brunner H.G.,
RA Kaesleriaenen H., Mulliken J.B., Tranenbjerg L., Brooks D.G.,
RA Cox G.P., Cruysberg J.R., Curtis M.A., Davenport S.L.H.,
RA Friedrich C.A., Kallila I., Krawczynski M.R., Latos-Bielenska A.,
RA Mkal S., Olsen B.R., Shimo N., Somer M., Vakkula M., Zlotogora J.,
RA Prockop D.J., Ala-Kokko L.;
RT "Splicing mutations of 54-bp exons in the COL11A1 gene cause Marshall
RT syndrome, but other mutations cause overlapping Marshall/Stickler
RT phenotypes.";
RL Am. J. Hum. Genet. 65:974-983(1999).
RN [3]
RP SEQUENCE OF 538-1806 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=89034222; PubMed=3182841;
RA Bernard M., Yoshida H., Rodriguez E., van der Rest M., Kimura T.,
RA Nimmiya Y., Olsen B.R., Ramirez F.;
RT "Cloning and sequencing of pro-alpha 1(XI) collagen cDNA
RT demonstrates that type XI belongs to the fibrillar class of collagens
RT and reveals that the expression of the gene is not restricted to
RT cartilaginous tissue.";
RL J. Biol. Chem. 263:17159-17166(1988).
RN [4]
RP ALTERNATIVE SPLICING.
RC TISSUE=Blood;
RX MEDLINE=95238468; PubMed=7721876;
RA Zhidkova N.I., Justice S.K., Mayne R.;
RT "Alternative mRNA processing occurs in the variable region of the
RT pro-alpha 1(XI) and pro-alpha 2(XI) collagen chains.";
RL J. Biol. Chem. 270:9486-9493(1995).
RN [5]
RP VARIANT STL2 VAL-625.
RX MEDLINE=97026296; PubMed=8872475;
RA Richards A.J., Yates J.R.W., Williams R., Payne S.J., Pope F.M.,
RA Scott J.D., Sneed M.P.;
RT "A family with Stickler syndrome type 2 has a mutation in the COL11A1
RT gene resulting in the substitution of glycine 97 by valine in
RT alpha-1(XI) collagen.";
RL Hum. Mol. Genet. 5:1339-1343(1996).
CC -1- FUNCTION: May play an important role in fibrillogenesis by
CC controlling lateral growth of collagen II fibrils.
CC -1- SUBUNIT: Trimers composed of three different chains: alpha 1(XI),
CC alpha 2(XI), and alpha 3(XI). Alpha 3(XI) is a post-translational
CC modification of alpha 1(XI). Alpha 1(XI) can also be found instead
CC of alpha 3(XI)=1(II).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Probable apoptosis inhibitor 2 (IAP-2).
 GN IAP2.
 OS Autographa californica nuclear polyhedrosis virus (AcMNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxId=46015;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C6;
 RX MEDLINE=94303173; PubMed=8030224;
 RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
 RT "The complete DNA sequence of Autographa californica nuclear
 polyhedrosis virus."
 RT Virology 203:586-605(1994).
 RL -1- SIMILARITY: Contains 1 BIR repeat.
 CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L23858; AAA66701.1; -.
 CC PIR: H72858; H72858.
 CC InterPro: IPR001370; BIR.
 CC InterPro: IPR001841; Znf_ring.
 CC Pfam: PF00653; BIR; 1.
 CC SMART: SMO0238; BIR; 1.
 CC SMART: SMO0184; RING; 1.
 CC PROSITE: PS01282; BIR_REPEAT_1; FALSE_NEG.
 CC PROSITE: PS01143; BIR_REPEAT_2; 1.
 CC PROSITE: PS00518; ZF_RING_1; FALSE_NEG.
 CC PROSITE: PS50089; ZF_RING_2; 1.
 CC KMW Apoptosis; Zinc-finger.
 FT REPEAT 85 152 BIR.
 FT ZN_RING 202 237 RING-TYPE.
 FT SEQUENCE 249 AA; 28621 MW; 4DE2825A792EE50 CRC64;
 SQ
 Query Match 79.5%; Score 35; DB 1; Length 249;
 Best Local Similarity 75.0%; Pred. No. 61;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSSPPEE 8
 DB 186 KPSPAPPAE 193
 RESULT 9,
 ID FING_CANFA STANDARD; PRT; 522 AA.
 AC Q28275; Q28276;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 15-MAR-2004 (Rel. 43, last annotation update)
 DE Fibronectin (FN) (Fragment).
 GN FN1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxId=9615;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Cartilage;
 RX MEDLINE=96324983; PubMed=8702559;
 RA MacLeod J.N., Burton-Wurster N., Gu D.N., Lust G.;
 RT "Fibronectin mRNA splice variant in articular cartilage lacks bases
 encoding the V, III-15, and I-10 protein segments.";

RL J. Biol. Chem. 271:18954-18960(1996).
 CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
 CC including collagen, fibrin, heparin, DNA, and actin. Fibronectins
 CC are involved in cell adhesion, cell motility, opsonization, wound
 CC healing, and maintenance of cell shape.
 CC -1- FUNCTION: Isoform 2 is probably involved in matrix organization of
 CC cartilage.
 CC -1- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
 CC variants, connected by 2 disulfide bonds near the carboxyl ends;
 CC to a lesser extent homodimers.
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Each of the "extra domain" and the connecting strand 3
 CC are present in some forms of fibronectin and absent from others;
 CC Name=1;
 CC IsoId=Q28275-1; Sequence=Displayed;
 CC Name=2; Synonyms=(V+C)-;
 CC IsoId=Q28275-2; Sequence=VSP_003251, VSP_003252;
 CC Note=lacks repeat 15 of fibronectin type-III, repeat 10 of
 CC fibronectin type-I, and the connecting strand 3;
 CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
 CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
 CC form), made by fibroblasts, epithelial and other cell types, is
 CC deposited as fibrils in the extracellular matrix. Isoform 2 is the
 CC major transcript in articular cartilage, but it is absent from
 CC liver.
 CC -1- PTM: Sulfated (By similarity).
 CC -1- SIMILARITY: Contains at least 4 fibronectin type III domains.
 CC -1- SIMILARITY: Contains at least 3 fibronectin type I domains.
 CC -----
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 CC -----
 CC EMBL: U52106; AAC48612.1; -.
 CC EMBL: U52105; AAC48611.1; -.
 CC HSP: P02751; 1FNH.
 CC InterPro: IPR000083; Fibnctn1.
 CC InterPro: IPR008957; FN_III-1like.
 CC InterPro: IPR003961; FN III.
 CC InterPro: IPR003962; FNIII_subd.
 CC Pfam: PF00039; fn1; 3.
 CC Pfam: PF00041; fn3; 3.
 CC PRINTS: PR00014; FNTYPEIII.
 CC SMART: SMO0058; FN1; 2.
 CC SMART: SMO0060; FN3; 3.
 CC PROSITE: PS01253; FIBRONECTIN_1; 2.
 CC KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
 CC Repeat; Sulfation; Alternative splicing.
 FT NON_TER 1
 FT DOMAIN 1
 FT DOMAIN <1 204 HEPARIN-BINDING 2 (BY SIMILARITY).
 FT DOMAIN 325 >522 FIBRIN-BINDING 2 (BY SIMILARITY).
 FT DOMAIN <1 25 FIBRONECTIN TYPE-III 13.
 FT DOMAIN 26 114 FIBRONECTIN TYPE-III 14.
 FT DOMAIN 115 204 FIBRONECTIN TYPE-III 15.
 FT DOMAIN 205 315 CONNECTING STRAND 3 (CS-3) (V REGION).
 FT DOMAIN 316 395 FIBRONECTIN TYPE-III 16.
 FT DOMAIN 417 461 FIBRONECTIN TYPE-I 10.
 FT DOMAIN 462 504 FIBRONECTIN TYPE-I 11.
 FT DOMAIN 506 >522 FIBRONECTIN TYPE-I 12.
 FT SITE 304 306 CELL ATTACHMENT SITE (POTENTIAL).
 FT DISULFID 419 448 BY SIMILARITY.
 FT DISULFID 446 458 BY SIMILARITY.
 FT DISULFID 464 491 BY SIMILARITY.
 FT DISULFID 489 501 BY SIMILARITY.
 FT DISULFID 508 >522 BY SIMILARITY.
 FT MOD_RES 509 509 SULFATION (POTENTIAL).
 FT CARBOHYD 321 N-LINKED (GLCNAC. . .) (BY SIMILARITY).

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CC CARBOHYD 277 277 O-LINKED (GALNAC. . .) (BY SIMILARITY).
CC CARBOHYD 278 278 O-LINKED (GALNAC. . .) (BY SIMILARITY).
CC VARSPLIC 205 205 D -> E (in isoform 2).
CC VARSPLIC 206 462 /FTid=VSP_003251.
CC VARSPLIC 206 462 Missing (in isoform 2).
CC VARSPLIC 206 462 /FTid=VSP_003252.
CC NON TER 522 522
CC SEQUENCE 522 AA; 57700 MW; DBID9A54C2BDAE26 CRC64;

Query Match 79.5%; Score 35; DB 1; Length 522;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 152 KPSSPPEE 159

RESULT 10
FINC HORSE STANDARD; PRT; 522 AA.
ID F1NC HORSE
AC Q28377; Q28378;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibronectin (FN) (Fragment).
GN FNI.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Liver;
RX MEDLINE=96324983; PubMed=8702559;
RA MacLeod J.N., Burton-Wurster N., Gu D.N., Lust G.;
RT "Fibronectin mRNA splice variant in articular cartilage lacks bases
RT encoding the V, III-15, and I-10 protein segments."
RL J. Biol. Chem. 271:18954-18960(1996).
CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
CC including collagen, fibrin, heparin, DNA, and actin. Fibronectins
CC are involved in cell adhesion, cell motility, opsonization, wound
CC healing, and maintenance of cell shape.
CC -1- FUNCTION: Isoform 2 is probably involved in matrix organization of
CC cartilage.
CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
CC TO A LESSER EXTENT HOMODIMERS.
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist. Each of the "extra
CC domain" and the connecting strand 3 are present in some forms of
CC fibronectin and absent in others;
CC Name=1;
CC Name=2;
CC IsoId=Q28377-1; Sequence=Displayed;
CC Name=2; Synonyms=(V+C)-;
CC Note=lacks repeat 15 of fibronectin type-III, repeat 10 of
CC fibronectin type-I, and the connecting strand 3;
CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
CC by hepatocytes. Cellular FN (soluble or cross-linked multimeric
CC forms), made by fibroblasts, epithelial and other cell types, is
CC deposited as fibrils in the extracellular matrix. Isoform 2 is the
CC major transcript in articular cartilage; very low levels in lymph
CC node, bone, aorta, and skin; absent from liver, spleen, placenta,
CC cardiac muscle, skeletal muscle, stomach, small intestine, and
CC kidney.
CC -1- PTM: Sulfated (By similarity).
CC -1- SIMILARITY: Contains at least 4 fibronectin type III domains.
CC -1- SIMILARITY: Contains at least 3 fibronectin type I domains.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U52107; AAC48613.1; -.
CC EMBL; U52108; AAC48614.1; -.
CC HSSP; P02751; FNI.
CC InterPro; IPR000083; Fibnctn1.
CC InterPro; IPR008957; FN III-like.
CC InterPro; IPR003964; FN III.
CC InterPro; IPR003963; FNI1_subd.
CC Pfam; PF00039; fn1_3.
CC Pfam; PF00041; fn3_3.
CC PRINTS; PR00014; FNTYPEIII.
CC SMART; SM00058; FNI; 2.
CC SMART; SM00060; FN3; 3.
CC PROSITE; PS01253; FIBRONECTIN 1; 2.
CC KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Cell adhesion;
CC Repeat; Sulfation; Alternative splicing.
CC Repeat; Sulfation; Alternative splicing.
CC NON TER 1 1
CC DOMAIN 1 204 HEPARIN-BINDING 2 (BY SIMILARITY).
CC DOMAIN 325 >522 FIBRIN-BINDING 2 (BY SIMILARITY).
CC DOMAIN 1 25 FIBRONECTIN TYPE-III 13.
CC DOMAIN 26 114 FIBRONECTIN TYPE-III 14.
CC DOMAIN 115 204 FIBRONECTIN TYPE-III 15.
CC DOMAIN 205 315 CONNECTING STRAND 3 (CS-3) (V REGION).
CC DOMAIN 316 395 FIBRONECTIN TYPE-III 16.
CC DOMAIN 417 461 FIBRONECTIN TYPE-I 10.
CC DOMAIN 462 504 FIBRONECTIN TYPE-I 11.
CC DOMAIN 506 >522 FIBRONECTIN TYPE-I 12.
CC SITE 304 306 CELL ATTACHMENT SITE (POTENTIAL).
CC SITE 419 448 BY SIMILARITY.
CC DISULFID 446 458 BY SIMILARITY.
CC DISULFID 464 491 BY SIMILARITY.
CC DISULFID 489 501 BY SIMILARITY.
CC MOD RES 515 515 SUPRION (POTENTIAL).
CC CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
CC CARBOHYD 277 277 O-LINKED (GALNAC. . .) (BY SIMILARITY).
CC CARBOHYD 278 278 O-LINKED (GALNAC. . .) (BY SIMILARITY).
CC VARSPLIC 205 205 D -> E (in isoform 2).
CC VARSPLIC 206 462 /FTid=VSP_003253.
CC VARSPLIC 206 462 Missing (in isoform 2).
CC VARSPLIC 206 462 /FTid=VSP_003254.
CC NON TER 522 522
CC SEQUENCE 522 AA; 57577 MW; 893E8AC895864D41 CRC64;

Query Match 79.5%; Score 35; DB 1; Length 522;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 152 KPSSPPEE 159

RESULT 11
ID ASPH BOVIN STANDARD; PRT; 754 AA.
AC Q28056;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aspartyl/asparaginyl beta-hydroxylase (EC 1.14.11.16) (Aspartate beta-
DE hydroxylase) (ASP beta-hydroxylase) (peptide-aspartate beta-
DE dioxygenase).
DB ASPH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.

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CC -----

DR EMBL, D25338; BAA04998.1; -.

DR EMBL, BC002536; AAH02536.1; -.

DR EMBL, BC029138; AAH29138.1; -.

DR EMBL, M64784; AAA36435.1; -.

DR PIR, JC2055; JC2055.

DR HSSP, P00512; 3PFK.

DR Genew, HGNC:8878; PFKP.

DR GK, Q01813; -.

DR MIM, 171840; -.

DR GO, GO:0005945; C:6-phosphofructokinase complex; NAS.

DR GO, GO:0003872; P:6-phosphofructokinase activity; TAS.

DR GO, GO:0006096; P:glycolysis; NAS.

DR InterPro, IPR000023; Pfructkinase.

DR Pfam, PF00365; PFK, 2.

DR PIRSF, PIRSF000533; PFK euk; 1.

DR PRINTS, PR00476; PHFCTKINASE.

DR Prodom, PD000707; Pfructkinase; 2.

DR PROSITE, PS00433; PHOSPHOFRUCTOKINASE; 2.

DR KINASE, TRANSFERASE; Glycolysis; Repeat; Allosteric enzyme; Phosphorylation; Magnesium; Multigene family.

KM CONFLICT 484 485 PG -> IP (IN REF. 3).

FT CONFLICT 498 498 MISSING (IN REF. 3).

FT CONFLICT 699 699 A -> B (IN REF. 3).

SO SEQUENCE 784 AA; 85596 MW; 22522EF7E9AF80F6 CRC64;

Query Match 79.5%; Score 35; DB 1; Length 784; Best Local Similarity 85.7%; Pred. No. 2.1e+02; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PSSPPE 8

Db 240 PSSPPE 246

RESULT 13

K6PP_MOUSE STANDARD; PRT; 784 AA.

ID K6PP_MOUSE

AC Q9WUJ3; Q9U186; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE 6-phosphofructokinase, type C (EC 2.7.1.11) (Phosphofructokinase 1) (Phosphohexokinase) (Phosphofructo-1-kinase isozyme C) (PFK-C).

GN PFKP OR PFKC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10990;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RA Gunasekera D., Kemp R.G.; Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RN (2)

RP SEQUENCE FROM N.A.

RA Sanchez-Martinez C., Estevez A.M., Argon J.J.; "Cloning, expression and properties of the phosphofructokinase C isozyme from acetles tumor cells."; Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

RN (3)

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6;

RA Gunasekera D., Kemp R.G.; "Genomic organization, 5' flanking region and tissue-specific expression of mouse phosphofructokinase C gene."; Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN (4)

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N-3; TISSUE=Mammary gland; MEDLINE=23388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Krausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusik A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grumwood J.W., Green E.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smolins D.E., Schnerch A., Schein J.E., Jones S.J.M., Maria W.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate.

CC -1- COFACTOR: Magnesium (By similarity).

CC -1- ENZYME REGULATION: Allosteric enzyme activated by ADP, AMP, or fructose bisphosphate and inhibited by ATP or citrate (By similarity).

CC -1- PATHWAY: Key control step of glycolysis.

CC -1- SIMILARITY: Belongs to the phosphofructokinase family. Two domains subfamily.

CC -----

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CC -----

DR EMBL, AF123533; AAD23571.1; -.

DR EMBL, Y19008; CAB64347.1; -.

DR EMBL, AF249893; AAF75700.1; -.

DR EMBL, AF250369; AAF75700.1; JOINED.

DR EMBL, AF250370; AAF75700.1; JOINED.

DR EMBL, AF250371; AAF75700.1; JOINED.

DR EMBL, AF250372; AAF75700.1; JOINED.

DR EMBL, AF251021; AAF75700.1; JOINED.

DR EMBL, BC006926; AAH06926.1; -.

DR HSSP, P00512; 3PFK.

DR MGD, MGI:1891833; PFKP.

DR GO, GO:0003872; P:6-phosphofructokinase activity; IDA.

DR InterPro, IPR000023; Pfructkinase.

DR Pfam, PF00365; PFK, 2.

DR PIRSF, PIRSF000533; PFK euk; 1.

DR PRINTS, PR00476; PHFCTKINASE.

DR Prodom, PD000707; Pfructkinase; 2.

DR PROSITE, PS00433; PHOSPHOFRUCTOKINASE; 2.

KM kinase, TRANSFERASE; Glycolysis; Repeat; Allosteric enzyme; Phosphorylation; Magnesium; Multigene family.

KW CONFLICT 180 180 T -> P (IN REF. 3).

FT CONFLICT 180 180

SO SEQUENCE 784 AA; 85455 MW; E9C5AABF26FCA65 CRC64;

Query Match 79.5%; Score 35; DB 1; Length 784; Best Local Similarity 85.7%; Pred. No. 2.1e+02; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PSSPPE 8

Db 239 PSSPPE 245

RESULT 14

K6PP_RAT STANDARD; PRT; 786 AA.

ID K6PP_RAT

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AC P47860;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 6-phosphofructokinase, type C (EC 2.7.1.11) (phosphofructokinase
DE 1) (phosphohexokinase) (phosphofructo-1-kinase isozyme C) (PFK-C)
DE (fragment).
GN PFKC OR PFKC OR PFK-C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=94148828; PubMed=8106374;
RA Gekakis N., Johnson R.C., Jenkins A., Mains R.E., Sul H.S.;
RT "Structure, distribution, and functional expression of the
RT phosphofructokinase C isozyme.";
RL J. Biol. Chem. 269:3348-3355(1994).
RN [2]
RP IDENTIFICATION OF PROBABLE FRAMESHIFT.
RA Balroch A.;
RL Unpublished observations (DEC-1995).
CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -1- COFACTOR: Magnesium.
CC -1- ENZYME REGULATION: Allosteric enzyme activated by ADP, AMP, or
CC fructose bisphosphate and inhibited by ATP or citrate.
CC -1- PATHWAY: Key control step of glycolysis.
CC -1- TISSUE SPECIFICITY: Expressed at high level in neuroendocrine
CC tissues.
CC -1- SIMILARITY: Belongs to the phosphofructokinase family. Two domains
CC subfamily.
CC -1- CAUTION: This is a conceptual translation; a frameshift was
CC introduced in position 25 to increase the similarity in the
CC N-terminal region with orthologs.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L25387; AAA1757.1; ALT_FRAME.
DR HSSP; P00512; 3PFK.
DR InterPro; IPR000023; Pfrfrckinase.
DR Pfam; PF00365; PFK; 2.
DR PIRSF; PIRSF000533; PFK euk; 1.
DR PRINTS; PR00476; PFRCKTNASE.
DR ProDom; PD000707; Pfrfrckinase; 2.
DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 2.
DR Kinase; Transferase; Glycolysis; Repeat; Allosteric enzyme;
KW Phosphorylation; Magnesium; Multigene family.
FT NON TER 1 1
SQ SEQUENCE 786 AA; 85601 MW; 9EE17A20A8F3B077 CRC64;

Query Match 79.5%; Score 35; DB 1; Length 786;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PSSPPEE 8
DB 238 PSSPPEE 244

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DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 6-phosphofructokinase, type C (EC 2.7.1.11) (phosphofructokinase
DE 1) (phosphohexokinase) (phosphofructo-1-kinase isozyme C) (PFK-C).
GN PFKC.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94164929; PubMed=8119919;
RA Li Y., Valaitis A.P., Latshaw S.P., Kwiatkowska D., Tripathi R.L.,
RA Campbell M.C., Kemp R.G.;
RT "Structure and expression of the cDNA for the C isozyme of
RT phosphofructo-1-kinase from rabbit brain.";
RL J. Biol. Chem. 269:5781-5787(1994).
CC -1- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate = ADP + D-
CC fructose 1,6-bisphosphate.
CC -1- COFACTOR: Magnesium.
CC -1- ENZYME REGULATION: Allosteric enzyme activated by ADP, AMP, or
CC fructose bisphosphate and inhibited by ATP or citrate.
CC -1- PATHWAY: Key control step of glycolysis.
CC -1- SIMILARITY: Belongs to the phosphofructokinase family. Two domains
CC subfamily.
CC -----
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CC -----
DR EMBL; U01154; AAA17707.1; -.
DR HSSP; P00512; 3PFK.
DR InterPro; IPR000023; Pfrfrckinase.
DR Pfam; PF00365; PFK; 2.
DR PIRSF; PIRSF000533; PFK euk; 1.
DR PRINTS; PR00476; PFRCKTNASE.
DR ProDom; PD000707; Pfrfrckinase; 2.
DR PROSITE; PS00433; PHOSPHOFRUCTOKINASE; 2.
DR Kinase; Transferase; Glycolysis; Repeat; Allosteric enzyme;
KW Phosphorylation; Magnesium; Multigene family.
SQ SEQUENCE 791 AA; 86349 MW; 3C10A36F29FDB8 CRC64;

Query Match 79.5%; Score 35; DB 1; Length 791;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PSSPPEE 8
DB 240 PSSPPEE 246

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RESULT 15
K6PP_RABIT STANDARD; PRT; 791 AA.
AC P47859;
DT 01-FEB-1996 (Rel. 33, Created)

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RESULT 16
DPOL_HSV21 STANDARD; PRT; 1240 AA.
ID DPOL_HSV21
AC P07938;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7.7).
OS Herpes simplex virus (type 2 / strain 186).
OC Viruses; dsDNA viruses; no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10312;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87277385; PubMed=3038677;
RA Tsurumi T., Maeno K., Nishiyama Y.;
RT "Nucleotide sequence of the DNA polymerase gene of herpes simplex

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RT Virus type 2 and comparison with the type 1 counterpart.;
RL Gene 52:129-137(1987).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + (DNA)(N).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -----
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CC -----
DR EMBL; M16321; AAA45853.1; -.
DR PIR; A27315; DJBE21.
DR InterPro; IPR006172; DNA_pol_B.
DR InterPro; IPR006134; DNA_pol_B_dom.
DR InterPro; IPR006133; DNA_pol_B_exo.
DR Pfam; PF00136; DNA_pol_B_1.
DR Pfam; PF03104; DNA_pol_B_exo; 1.
DR PRINTS; PR00106; DNAPOLB.
DR SMART; SM00486; POLBC; 1.
DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
DR Transferrase; DNA-directed DNA polymerase; DNA replication;
DR DNA-binding; Nuclear protein.
DR KW DNA-binding; Nuclear protein.
SQ SEQUENCE 1240 AA; 13735 MW; 1CDABD1DF180E CRC64;

Query Match
Best Local Similarity 85.7%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PSSPPEE 8
Db 798 PSSPPEE 804

RESULT 17
TABP_HUMAN : STANDARD; PRT; 1729 AA.
ID TABP_HUMAN : STANDARD; PRT; 1729 AA.
AC Q9C0C2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 182 kDa tankyrase 1-binding protein.
GN TNKS1BP1 OR TAB182 OR KIAA1741.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21082932; PubMed=11214970;
RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT "The telomeric poly(ADP-ribose) polymerase, tankyrase 1, contains
RT multiple binding sites for telomeric repeat binding factor 1 (TRF1)
RT and a novel acceptor, 182-kDa tankyrase-binding protein (TAB182).";
RL J. Biol. Chem. 277:14116-14126(2002).
RN (12)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21082932; PubMed=11214970;
RA Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
RT "The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:347-355(2000).
RN (3)
RP SEQUENCE OF 495-1729 FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22579292; PubMed=12693554;

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RA Jikuya H., Takano J., Kikuno R., Hirosewa M., Nagase T., Nomura N.,
RA Ohara O.;
RT "Characterization of long cDNA clones from human adult spleen. II. The
RT complete sequences of 81 cDNA clones.";
RL DNA Res. 10:49-57(2003).
CC -1- SUBUNIT: Binds to the ANK repeat domain of TNKS1 and TNKS2.
CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic. Colocalizes with
CC chromosomes during mitosis, and in the cytoplasm with cortical
CC actin.
CC -1- TISSUE SPECIFICITY: Detected in testis, ovary, lung, skeletal
CC muscle, heart, prostate and pancreas, and at very low levels in
CC brain and peripheral blood leukocytes.
CC -1- PTM: ADP-ribosylated by TNKS1 (in vitro).
CC -1- CAUTION: Ref 3 sequence differs from that shown due to frameshifts
CC in position 1071, 1097 and 1467.
CC -----
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CC -----
DR EMBL; AF441771; AAM1553.1; -.
DR EMBL; AB051528; BAB21832.2; ALT_INT.
DR EMBL; AK074113; BAB84939.1; ALT_FRAME.
DR Genew; HGNC:19081; TNKS1BP1.
DR GK; Q9C0C2; -.
DR MIM; 607104; -.
DR GO; GO:0005737; Cytoplasm; NAS.
DR GO; GO:0005724; C-nuclear telomeric heterochromatin; NAS.
DR GO; GO:0005634; C-nucleus; NAS.
DR GO; GO:0030506; F-ankyrin binding; NAS.
DR GO; GO:0019899; F-enzyme binding; NAS.
DR GO; GO:0007004; P-telomerase-dependent telomere maintenance; NAS.
DR InterPro; IPR008979; Gal blind like.
KW Nuclear protein; Chromosomal protein; ADP-ribosylation.
RN (1)
RP SEQUENCE 1729 AA; 181814 MW; C65F38FA37045C4A CRC64;
FT DOMAIN 2 103
FT DOMAIN 127 767
FT DOMAIN 210 1572
FT DOMAIN 1010 1340
FT DOMAIN 1450 1542
FT DOMAIN 1572 1729
FT DOMAIN 1629 1635
FT DOMAIN 1723 1729
FT CONFICT 84 84
FT CONFICT 322 322
FT CONFICT 388 388
FT CONFICT 554 554
FT CONFICT 604 604
FT CONFICT 1450 1450
SQ SEQUENCE 1729 AA; 181814 MW; C65F38FA37045C4A CRC64;

Query Match
Best Local Similarity 75.0%; Pred. No. 4.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSSPPEE 8
Db 366 KPSSPPEE 373

RESULT 18
BAZA_HUMAN : STANDARD; PRT; 1878 AA.
ID BAZA_HUMAN : STANDARD; PRT; 1878 AA.
AC Q9UIF9; Q00536; O15030; Q96H26;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bromodomain adjacent to zinc finger domain 2A (Transcription
DE termination factor-1 interacting protein 5) (TFP-I interacting protein
DE 5) (Tfips) (hMALp3).

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GN BAZZA OR TIPS OR KIA0314.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=20130112; PubMed=10662543;
 RA Jones M.H., Hamana N., Nezu J.-I., Shizane M.;
 RT "a novel family of bromodomain genes.";
 RL Genomics 63:40-45(2000).
 RN [2]
 RP SEQUENCE OF 332-738 FROM N.A.
 RC TISSUE=Lung;
 RA Jansa P., Grunnet I.;
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 639-1878 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97349984; PubMed=9205841;
 RA Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT Prediction of the coding sequences of unidentified human genes. VII.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 4:141-150(1997).
 RN [4]
 RP SEQUENCE OF 1035-1878 FROM N.A.
 RC TISSUE=Lymph;
 RX MEDLINE=23388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diatchenko L., Marais K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schuetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshylyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulys S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scheraga A., Schein J.E., Jones S.J.M., Matra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: May play a role in transcriptional regulation
 CC interacting with ISWI. May serve a specific role in maintaining or
 CC altering the chromatin structure of the rDNA locus (By
 CC similarity).
 CC -1- SUBUNIT: Together with ISWI/SNP2h, it forms a complex termed NORC
 CC (nucleolar remodeling complex).
 CC -1- SUBCELLULAR LOCATION: Nuclear. Colocalizes with the basal RNA
 CC POLYMERASE I transcription factor UBF in the nucleolus.
 CC -1- TISSUE SPECIFICITY: Expressed at moderate levels in most tissues
 CC analyzed, including heart, brain, placenta, lung, skeletal muscle,
 CC kidney and pancreas.
 CC -1- SIMILARITY: Belongs to the WAF family.
 CC -1- SIMILARITY: Contains 4 A.T hook DNA-binding repeats.
 CC -1- SIMILARITY: Contains 1 bromodomain.
 CC -1- SIMILARITY: Contains 1 DDT domain.
 CC -1- SIMILARITY: Contains 1 methyl-binding (MBD) domain.
 CC -1- SIMILARITY: Contains 1 PBD-type zinc finger.
 CC -----
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 CC -----
 CC EMBL; AB032254; BAA89211.1; -;
 CC DR EMBL; AF000422; AAB60864.1; -;
 CC DR EMBL; AB002312; BAA20773.1; -;
 CC DR EMBL; BC008965; AAB08965.1; -;
 CC DR HSSP; Q92831; IB91.
 CC DR Genew; HGNC:962; BAZ2A.
 CC MIM; 605682; -;
 CC DR GO; GO:0005731; C:nucleolus organizer complex; NAS.
 CC DR GO; GO:0003677; F:DNA binding; NAS.
 CC DR GO; GO:0030528; F:transcription regulator activity; NAS.
 CC DR GO; GO:0006338; P:chromatin modeling; NAS.
 CC DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
 CC DR InterPro; IPR000637; AT hook.
 CC DR InterPro; IPR001487; Bromodomain.
 CC DR InterPro; IPR004022; DDT_dom.
 CC DR InterPro; IPR001739; Methyl-Cpg_bind.
 CC DR InterPro; IPR001965; Znf PHD.
 CC DR Pfam; PF02178; AT hook; 4.
 CC DR Pfam; PF00439; bromodomain; 1.
 CC DR Pfam; PF02791; DDT; 1.
 CC DR Pfam; PF01429; MBD; 1.
 CC DR Pfam; PF00628; PHD; 1.
 CC DR PRINTS; PR00503; BROMODOMAIN.
 CC DR SMART; SM00384; AT hook; 4.
 CC DR SMART; SM00297; BROMO; 1.
 CC DR SMART; SM00571; DDT; 1.
 CC DR SMART; SM00391; MBD; 1.
 CC DR SMART; SM00249; PHD; 1.
 CC DR PROSITE; PS00633; BROMODOMAIN_1; FALSE_NEG.
 CC DR PROSITE; PS50014; BROMODOMAIN_2; 1.
 CC DR PROSITE; PS50837; DDT; 1.
 CC DR PROSITE; PS01359; ZF_PHD_1; FALSE_NEG.
 CC DR PROSITE; PS50016; ZF_PHD_2; 1.
 CC DR PROSITE; PS50016; ZF_PHD_2; 1.
 CC KW Nuclear protein; Repeat; DNA-binding.
 CC FT DOMAIN 525 574
 CC FT DNA_BIND 622 634 A.T HOOK 1.
 CC FT DNA_BIND 643 655 A.T HOOK 2.
 CC FT DOMAIN 821 866 DDT.
 CC FT DNA_BIND 1159 1171 A.T HOOK 3.
 CC FT DNA_BIND 1377 1389 A.T HOOK 4.
 CC FT ZN_FING 1649 1699 PHD-TYPE.
 CC FT DOMAIN 1783 1853 BROMODOMAIN.
 CC FT DOMAIN 633 772 LYS-RICH.
 CC FT DOMAIN 666 765 COILED COIL (POTENTIAL).
 CC FT DOMAIN 1185 1250 GLU-RICH.
 CC FT DOMAIN 1263 1384 PRO-RICH.
 CC FT DOMAIN 1732 1735 POLY-ARG.
 CC FT DOMAIN 574 700 L->V (IN REF. 2).
 CC FT CONFLICT 700 700 L->Q (IN REF. 2 AND 3).
 CC FT CONFLICT 720 720 H->Q (IN REF. 2 AND 3).
 CC FT CONFLICT 727 738 SKAKKKKKTKQ->KIRKKKKKKKK (IN REF.
 CC FT CONFLICT 727 738 2).
 CC FT CONFLICT 785 785 K->R (IN REF. 3).
 CC FT CONFLICT 951 951 P->L (IN REF. 3).
 CC FT CONFLICT 1005 1006 GR->EG (IN REF. 3).
 CC FT CONFLICT 1035 1037 IAA->GIR (IN REF. 4).
 CC FT CONFLICT 1163 1163 G->S (IN REF. 1).
 CC FT CONFLICT 1166 1166 R->L (IN REF. 1).
 CC FT CONFLICT 1172 1172 S->F (IN REF. 1).
 CC FT CONFLICT 1178 1178 L->F (IN REF. 1).
 CC FT CONFLICT 1202 1202 A->V (IN REF. 1).
 CC FT CONFLICT 1292 1292 P->L (IN REF. 1).
 CC FT CONFLICT 1295 1295 L->F (IN REF. 1).
 CC FT CONFLICT 1313 1313 P->L (IN REF. 1).
 CC FT CONFLICT 1407 1410 MISSING (IN REF. 4).
 CC FT CONFLICT 1416 1416 R->P (IN REF. 1).
 CC FT CONFLICT 1541 1541 R->P (IN REF. 1).
 CC FT CONFLICT 1571 1571 E->K (IN REF. 1).


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FT CONFLICT 1616 1616 V -> I (IN REF. 1).
FT CONFLICT 1622 1622 E -> Q (IN REF. 1).
FT CONFLICT 1629 1629 Q -> H (IN REF. 1).
FT CONFLICT 1636 1636 Q -> H (IN REF. 1).
FT CONFLICT 1739 1739 R -> K (IN REF. 1).
FT CONFLICT 1754 1754 G -> R (IN REF. 1).
SQ SEQUENCE 1878 AA; 208480 MW; 400970CA68234317 CRC64;

Query Match 79.5%; Score 35; DB 1; Length 1878;
Best Local Similarity 85.7%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 PSSPPE 8
Db 1274 PSSPPE 1280

RESULT 19
PTPD_HUMAN STANDARD; PRT; 1912 AA.
AC P23468;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase delta precursor (BC 3.1.3.48) (R-PTP-
delta).
GN PTPRD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.
RX MEDLINE=9520468; PubMed=7896816;
RA Pullido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;
RT "Molecular characterization of the human transmembrane protein-
RT tyrosine phosphatase delta. Evidence for tissue-specific expression of
RT alternative human transmembrane protein-tyrosine phosphatase delta
RT isoforms."
RT J. Biol. Chem. 270:6722-6728(1995).
RL (2)
RN SEQUENCE OF 390-1912 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=91006018; PubMed=2170109;
RA Krueger N.X., Streuli M., Saito H.;
RT "Structural diversity and evolution of human receptor-like protein
RT tyrosine phosphatases."
RL EMBL J. 9:3241-3252(1990).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=P23468-1; Sequence=Displayed;
CC Name=2; Synonyms=Kidney;
CC IsoId=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
CC Name=3; Synonyms=Fetal brain;
CC IsoId=P23468-3; Sequence=VSP_005150;
CC -1- FROM THE TRANSMEMBRANE SEGMENT.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: Contains 8 fibronectin type III domain.
CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC -----
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CC EMBL: I38929; AAC41749.1; -
DR EMBL: X54133; CA38068.1; -
DR EMBL: A56178; A56178.
DR HSSP: P18052; 1YFO.
DR Genew: HGNC:9668; PTPRD.
DR MIM: 601598; -
DR CO: GO:0005887; C: integral to plasma membrane; TAS.
DR CO: GO:0005001; F: transmembrane receptor protein tyrosine pho. . .; TAS.
DR GO: GO:0006470; P: protein amino acid dephosphorylation; TAS.
DR GO: GO:0007185; P: transmembrane receptor protein tyrosine pho. . .; TAS.
DR InterPro: IPR008957; FN III-1like.
DR InterPro: IPR003964; FN III.
DR InterPro: IPR003962; FNIII subd.
DR InterPro: IPR007110; Ig-1like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR000387; Tyr_P.
DR InterPro: IPR000242; Tyr_PP.
DR Pfam: PF00047; fn3; 8.
DR Pfam: PF00047; Ig; 3.
DR Pfam: PF00102; Y_phosphatase; 2.
DR PRINTS: PR00014; ENTPEPIT.
DR SMART: SM00700; PRTYPHPTASE.
DR SMART: SM00060; FN3; 8.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00194; PTPC; 2.
DR PROSITE: PS00835; IG_LIKE; 3.
DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE: PS50056; TYR_PHOSPHATASE_2; 2.
DR PROSITE: PS50055; TYR_PHOSPHATASE_PTP; 2.
KM Hydrolyase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 1912
FT DOMAIN 21 1265
FT TRANSMEM 1266 1290
FT DOMAIN 1291 1912
FT DOMAIN 126 114
FT DOMAIN 126 224
FT DOMAIN 236 318
FT DOMAIN 320 414
FT DOMAIN 417 513
FT DOMAIN 516 606
FT DOMAIN 609 708
FT DOMAIN 711 822
FT DOMAIN 825 916
FT DOMAIN 918 1017
FT DOMAIN 1020 1137
FT DOMAIN 1375 1618
FT DOMAIN 1619 1912
FT ACT_SITE 1553 1553
FT ACT_SITE 1844 1844
FT SITE 1175 1178
FT CARBOHYD 254 254
FT CARBOHYD 299 299
FT CARBOHYD 724 724
FT CARBOHYD 832 832
FT VARSPLIC 181 189
FT VARSPLIC 226 229
FT VARSPLIC 775 783
FT VARSPLIC 609 1137
FT MUTAGEN 1178 1178
SQ SEQUENCE 1912 AA; 214759 MW; 3A8CB0D32182E26 CRC64;

Query Match 79.5%; Score 35; DB 1; Length 1912;
Best Local Similarity 62.5%; Pred. No. 5.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KPSPPEE 8
 Db 608 KPSPAPPD 615

RESULT 20
 PTNS_HUMAN
 ID PTNS_HUMAN STANDARD; PRT; 1948 AA.
 AC Q13332; Q15718; Q16341;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Receptor-tyrosine protein phosphatase 5 precursor (EC 3.1.3.48)
 DE (R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).
 GN PTPRS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal brain;
 RX MEDLINE=96102179; PubMed=8524829;
 RA Pulido R., Serra-Pages C., Tang M., Streuli M.;
 RT "The LAR/PTP delta/PTP sigma subfamily of transmembrane protein-
 RT tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma
 RT isoforms are expressed in a tissue-specific manner and associate with
 RT the LAR-interacting protein LIP-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690 (1995).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96255038; PubMed=8992885;
 RA Endo N., Rutledge S.J., Opas E.E., Vogel R., Rodan G.A., Schmidt A.;
 RT "Human protein tyrosine phosphatase-sigma: alternative splicing and
 RT inhibition by bisphosphonates.";
 RL J. Bone Miner. Res. 11:535-543 (1996).
 RN
 RP SEQUENCE OF 1-126 FROM N.A.
 RA Lameudin J.E., McCreedy P.M., Skowronski B., Viswanathan V.,
 RA Burkhardt-Schulter K., Gordon L., Dias J., Ramirez M., Stijlwegen S.,
 RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J., Liu S.,
 RA Danganan L., Eriler A., Christensen M., Georgescu A., Avila J., Liu S.,
 RA Attix C., Andrease T., Frankheim M., Amico-Keller G., Coeffield J.,
 RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 RA Olsen A.S., Carraro A.V.;
 RT "Sequence analysis of a 2.5 Mb region in 19p13.3.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE OF 1503-1589 FROM N.A.
 RX MEDLINE=92119637; PubMed=1370651;
 RA Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh F., Hinoda Y.,
 RA Imai K., Yachi A.;
 RT "Protein-tyrosine phosphatase expression in pre-B cell NALM-6.";
 RL Cancer Res. 52:737-740 (1992).
 CC -1- FUNCTION: Interacts with LAR-interacting protein LIP-1.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Comment=Additional isoforms seem to exist;
 CC Name=PTPS;
 CC IsoId=Q13332-1; Sequence=Displayed;
 CC Name=PTPS-MEA;
 CC IsoId=Q13332-2; Sequence=VSP_050021;
 CC Name=PTPS-MEB;
 CC IsoId=Q13332-3; Sequence=VSP_050022, VSP_050026, VSP_050027;
 CC Name=PTPS-MEC;
 CC IsoId=Q13332-4; Sequence=VSP_050024;
 CC Name=PTPS-P4-7;
 CC IsoId=Q13332-5; Sequence=VSP_050023, VSP_050025;

CC -1- TISSUE SPECIFICITY: Detected in all tissues tested except for
 CC placenta and liver.
 CC -1- SIMILARITY: BELONGS TO THE RECEPTOR CLASS OF THE PROTEIN-TYROSINE
 CC PHOSPHATASE FAMILY.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.
 CC -1- SIMILARITY: Contains 8 fibronectin type III domain.
 CC -1- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -----
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 CC -----
 DR EMBL; U35234; AAC50299.1; -;
 DR EMBL; U40317; AAC50567.1; -;
 DR EMBL; AC005790; AAC62832.1; -;
 DR EMBL; S78080; AAB21146.2; -;
 DR HSSP; P18052; IYFO.
 DR Genew; HGNC:9681; PTPRS.
 DR MIM; 601576; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
 DR Interpro; IPR008957; FN III-like.
 DR Interpro; IPR003961; FN III.
 DR Interpro; IPR003962; FNIII subd.
 DR Interpro; IPR007110; Ig-like.
 DR Interpro; IPR003598; Ig_c2.
 DR Interpro; IPR000387; Tyr_phosphatase.
 DR Interpro; IPR000242; Tyr_PP.
 DR Pfam; PF00041; fn3; 8.
 DR Pfam; PF00047; ig; 3.
 DR Pfam; PF00102; Y_phosphatase; 2.
 DR PRINTS; PRO0014; ERTYPRHII.
 DR PRINTS; PRO0700; ERTYPRHIIASE.
 DR SMART; SM00060; FN3; 7.
 DR SMART; SM00408; IGC2; 3.
 DR SMART; SM00194; PTPC; 2.
 DR PROSITE; PSS0835; IG LIKE; 3.
 DR PROSITE; PSS0383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PSS0056; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 2.
 KM Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
 KM Cell adhesion; Immunoglobulin domain; Alternative splicing; Repeat.
 FT FT SIGNAL 1 29
 FT CHAIN 30 1948
 FT
 FT DOMAIN 30 1282
 FT TRANSLEM 1283 1303
 FT DOMAIN 1304 1948
 FT DOMAIN 33 123
 FT DOMAIN 135 233
 FT DOMAIN 245 327
 FT DOMAIN 329 423
 FT DOMAIN 426 522
 FT DOMAIN 525 615
 FT DOMAIN 618 717
 FT DOMAIN 720 831
 FT DOMAIN 834 926
 FT DOMAIN 928 1033
 FT DOMAIN 1036 1151
 FT DOMAIN 1393 1648
 FT DOMAIN 1680 1930
 FT DOMAIN 641 644
 FT DISULFID 54 107
 FT DISULFID 156 216
 FT DISULFID 266 311
 FT ACT_SITE 1589 1589
 FT ACT_SITE 1880 1880

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FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 733 733 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 940 940 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 198 Missing (in isoform PTPS-MEA).
FT VARSPLIC 236 239 Missing (in isoform PTPS-MEB).
FT VARSPLIC 617 1034 Missing (in isoform PTPS-F4-7).
FT VARSPLIC 784 792 Missing (in isoform PTPS-MEC).
FT VARSPLIC 1035 1035 V -> I (in isoform PTPS-F4-7).
FT VARSPLIC 1350 1365 Missing (in isoform PTPS-MEB).
FT VARSPLIC 1366 1366 S -> G (in isoform PTPS-MEB).
FT CONFLICT 310 310 /FTID=VSP_050027.
FT CONFLICT 428 429 T -> HP (IN REF. 2).
FT CONFLICT 742 745 LGPV -> RSPA (IN REF. 2).
FT CONFLICT 763 773 GAEGRP -> RREGRGRS (IN REF. 2).
FT CONFLICT 910 910 R -> P (IN REF. 2).
FT CONFLICT 986 995 AAEPAENAV -> GLSRARRTL (IN REF. 2).
FT CONFLICT 1195 1196 TV -> SL (IN REF. 2).
FT CONFLICT 1431 1431 E -> S (IN REF. 2).
FT CONFLICT 1546 1546 E -> D (IN REF. 4).
FT CONFLICT 1587 1587 V -> A (IN REF. 4).
FT CONFLICT 1705 1705 N -> K (IN REF. 2).
SQ SEQUENCE 1948 AA; 217080 MM; 7DC049EC03171136 CRC64;

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Query Match 79.5%; Score 35; DB 1; Length 1948;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 KPSPPPE 8
Db 617 KPSAPRD 624

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RESULT 21
FINC BOVIN STANDARD; PRT; 2265 AA.
AC P07589;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Fibronectin (FN).
GN FNI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=87054047; PubMed=3780752;
RA Skorstengaard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.;
RT "Complete primary structure of bovine plasma fibronectin.";
RL Eur. J. Biochem. 161:441-453(1986).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=83117805; PubMed=6218503;
RA Petersen T.E., Thorgersen H.C., Skorstengaard K., Vibe-Pedersen K.,
RA Sahl P., Sottrup-Jensen L., Magnusson S.;
RT "Partial primary structure of bovine plasma fibronectin: three types
RT of internal homology.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).
RN [3]
RP SEQUENCE OF 2170-2265 FROM N.A.
RX MEDLINE=83221567; PubMed=6304699;
RA Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
RT "Isolation and characterization of cDNA clones for human and bovine

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RT fibronectins.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).
CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds
CC including collagen, fibrin, heparin, DNA, and actin. Fibronectins
CC are involved in cell adhesion, cell motility, opsonization, wound
CC healing, and maintenance of cell shape.
CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED
CC VARIANTS, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS;
CC TO A LESSER EXTENT HOMODIMERS.
CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced. Each of the "extra
CC domain" and the connecting strand 3 are present in some forms of
CC fibronectin and absent in others;
CC Name=1;
CC -1- IsoId=P07589-1; Sequence=displayed;
CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
CC forms), made by fibroblasts, epithelial and other cell types, is
CC deposited as fibrils in the extracellular matrix.
CC -1- PTM: Sulfated (by similarity).
CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
CC -1- SIMILARITY: Contains 15 fibronectin type III domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; K00800; AAA30521.2; -.
DR PIR; A26452; FNBO.
DR HSSP; P02751; 2FN2.
DR InterPro; IPR006209; BGF_1like.
DR InterPro; IPR000083; FibrinctnI.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR003962; FnnII_subd.
DR Pfam; PR00039; fnI; 12.
DR Pfam; PR00040; fn2; 2.
DR Pfam; PR00041; fn3; 15.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 14.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Phosphorylation;
KW Sulfation; Cell adhesion; Repeat; Alternative splicing;
KW Pyrolydione carboxylic acid.
FT MOD_RES 1 1 PYROLYDIONE CARBOXYLIC ACID.
FT DOMAIN 21 241 FIBRIN- AND HEPARIN-BINDING 1.
FT DOMAIN 277 577 COLLAGEN-BINDING.
FT DNA_BIND 876 1141 CELL-ATTACHMENT.
FT DOMAIN 1236 1509 HEPARIN-BINDING 2.
FT DOMAIN 1600 1870 FIBRIN-BINDING 2.
FT DOMAIN 1991 2216 FIBRONECTIN TYPE-I 1.
FT DOMAIN 19 59 FIBRONECTIN TYPE-I 2.
FT DOMAIN 64 107 FIBRONECTIN TYPE-I 3.
FT DOMAIN 108 151 FIBRONECTIN TYPE-I 4.
FT DOMAIN 153 197 FIBRONECTIN TYPE-I 5.
FT DOMAIN 198 242 FIBRONECTIN TYPE-I 6.
FT DOMAIN 275 314 FIBRONECTIN TYPE-II 1.
FT DOMAIN 314 373 FIBRONECTIN TYPE-II 2.
FT DOMAIN 374 438

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FT DOMAIN 437 480 FIBRONECTIN TYPE-I 7.
 FT DOMAIN 485 527 FIBRONECTIN TYPE-I 8.
 FT DOMAIN 528 571 FIBRONECTIN TYPE-I 9.
 FT DOMAIN 578 669 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 688 778 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 779 874 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 875 964 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 965 1054 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 1055 1141 FIBRONECTIN TYPE-III 6.
 FT DOMAIN 1142 1234 FIBRONECTIN TYPE-III 7.
 FT DOMAIN 1235 1325 FIBRONECTIN TYPE-III 8.
 FT DOMAIN 1326 1415 FIBRONECTIN TYPE-III 9.
 FT DOMAIN 1416 1509 FIBRONECTIN TYPE-III 10.
 FT DOMAIN 1510 1599 FIBRONECTIN TYPE-III 11.
 FT DOMAIN 1600 1691 FIBRONECTIN TYPE-III 12.
 FT DOMAIN 1692 1780 FIBRONECTIN TYPE-III 13.
 FT DOMAIN 1781 1870 FIBRONECTIN TYPE-III 14.
 FT DOMAIN 1871 1990 CONNECTING STRAND 3 (CS-3) (V REGION).
 FT DOMAIN 1982 2061 FIBRONECTIN TYPE-III 15.
 FT DOMAIN 2083 2127 FIBRONECTIN TYPE-I 10.
 FT DOMAIN 2128 2170 FIBRONECTIN TYPE-I 11.
 FT DOMAIN 2172 2215 FIBRONECTIN TYPE-I 12.
 FT SITE 1493 1495 CELL ATTACHMENT SITE.

FT DISULFID 21 47
 FT DISULFID 45 56
 FT DISULFID 66 94
 FT DISULFID 92 104
 FT DISULFID 110 138
 FT DISULFID 136 148
 FT DISULFID 155 184
 FT DISULFID 182 194
 FT DISULFID 200 229
 FT DISULFID 227 239
 FT DISULFID 277 304
 FT DISULFID 302 311
 FT DISULFID 329 355
 FT DISULFID 343 370
 FT DISULFID 389 415
 FT DISULFID 403 430
 FT DISULFID 439 467
 FT DISULFID 465 477
 FT DISULFID 487 514
 FT DISULFID 512 524
 FT DISULFID 530 558
 FT DISULFID 556 568
 FT DISULFID 2085 2114
 FT DISULFID 2112 2124
 FT DISULFID 2130 2157
 FT DISULFID 2155 2167
 FT DISULFID 2174 2200
 FT DISULFID 2198 2209
 FT DISULFID 2246 2246
 FT DISULFID 2250 2250
 FT MOD_RES 845 845
 FT MOD_RES 850 850
 FT CARBOHYD 399 399
 FT CARBOHYD 497 497
 FT CARBOHYD 511 511
 FT CARBOHYD 846 846
 FT CARBOHYD 976 976
 FT CARBOHYD 1213 1213
 FT CARBOHYD 1987 1987
 FT CARBOHYD 1943 1943
 FT CARBOHYD 1944 1944
 FT MOD_RES 2263 2263
 SQ SEQUENCE 2265 AA; 249557 MW; C2D21D486F498D5C CRC64;

Query Match 79.5%; Score 35; DB 1; Length 2265;
 Best Local Similarity 75.0%; Pred. No. 6.4e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1818 KEGSPPRE 1825
 RESULT 22
 FINE_HUMAN STANDARD; PRT; 2386 AA.
 ID P02751; Q95609; Q95610; Q14312; Q14325; Q14326; Q86T27; Q81V18;
 AC Q96KP7; Q96KP8; Q96KP9; Q9H1B8; Q9HAP3; Q9UMK2;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Fibronectin precursor (FN) (Cold-insoluble globulin) (ClG).
 GN FN1 OR FN.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=21600194; PubMed=11737888;
 RA Schor S.L., Schor A.M.;
 RT "Phenotypic and genetic alterations in mammary stroma: implications
 RT for tumour progression.";
 RL Breast Cancer Res. 3:373-379(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 3; 7 AND 10).
 RC TISSUE=Cervix;
 RA Ansoorge W., Krieger S., Regiert T., Rittmuller C., Schwager B.,
 RA Mewes H.-W., Weil B., Amid C., Osanger A., Fobo G., Han M.,
 RA Wiemann S.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-38 FROM N.A.
 RX MEDLINE=87030890; PubMed=3770189;
 RA Gutman A., Yamada K.M., Kornblith A.R.;
 RT "Human fibronectin is synthesized as a pre-propolypeptide.";
 RL FEBS Lett. 207:145-148(1986).
 RN [4]
 RP SEQUENCE OF 1-49 FROM N.A.
 RX MEDLINE=87175578; PubMed=3031656;
 RA Dean D.C., Bowls C.L., Bourgeois S.;
 RT "Cloning and analysis of the promoter region of the human fibronectin
 RT gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:1876-1880(1987).
 RN [5]
 RP SEQUENCE OF 28-2386 FROM N.A. (ISOFORM 3).
 RX MEDLINE=85284965; PubMed=2992939;
 RA Kornblith A.R., Umezawa K., Vibe-Pedersen K., Baralle F.E.;
 RT "Primary structure of human fibronectin: differential splicing may
 RT generate at least 10 polypeptides from a single gene.";
 RL EMBO J. 4:1755-1759(1985).
 RN [6]
 RP SEQUENCE OF 103-481 AND 2228-2386 FROM N.A. (ISOFORMS 1; 3; 8 AND 9).
 RC TISSUE=Peripheral blood T-cell, and umbilical vein endothelial cells;
 RA Godfrey H.P., Ebrahim A.A.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 973-2386 FROM N.A. (ISOFORM 3).
 RX MEDLINE=84272258; PubMed=6462919;
 RA Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
 RT "Human fibronectin: cell specific alternative mRNA splicing generates
 RT polypeptide chains differing in the number of internal repeats.";
 RL Nucleic Acids Res. 12:5853-5868(1984).
 RN [8]
 RP SEQUENCE OF 1232-1782 FROM N.A. (ISOFORM 7).
 RX MEDLINE=88233940; PubMed=3375063;
 RA Paolletta G., Henchcliffe C., Sebastio G., Baralle F.E.;
 RT "Sequence analysis and in vivo expression show that alternative
 RT splicing of ED-B and ED-A regions of the human fibronectin gene are
 RT independent events.";
 RL Nucleic Acids Res. 16:3545-3557(1988).
 RN [9]
 RP SEQUENCE OF 1257-1365 FROM N.A. (ISOFORM 11).

RX MEDLINE=88041070; PubMed=2478690;
 RA Guttman A., Kornblith A.R.;
 RT "Identification of a third region of cell-specific alternative
 RT splicing in human fibronectin mRNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7179-7182(1987).
 RN [10]
 RP SEQUENCE OF 1441-1548.
 RX MEDLINE=82265604; PubMed=7050098;
 RA Pierschbacher W.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.
 RT "The cell attachment domain of fibronectin. Determination of the
 RT primary structure.";
 RL J. Biol. Chem. 257:9593-9597(1982).
 RN [11]
 RP SEQUENCE OF 1448-1540 FROM N.A.
 RX MEDLINE=83290929; PubMed=6689418;
 RA Oldberg A., Linney E., Ruoslahti E.;
 RT "Molecular cloning and nucleotide sequence of a cDNA clone coding for
 RT the cell attachment domain in human fibronectin.";
 RL J. Biol. Chem. 258:10193-10196(1983).
 RN [12]
 RP SEQUENCE OF 1448-1540 FROM N.A.
 RX MEDLINE=86111901; PubMed=3003095;
 RA Oldberg A., Ruoslahti E.;
 RT "Evolution of the fibronectin gene. Exon structure of cell attachment
 RT domain.";
 RL J. Biol. Chem. 261:2113-2116(1986).
 RN [13]
 RP SEQUENCE OF 1594-2386 FROM N.A. (ISOFORM 1).
 RX MEDLINE=85280409; PubMed=592573;
 RA Bernard M.P., Kolbe M., Weill D., Chu M.-L.;
 RT "Human cellular fibronectin: comparison of the carboxyl-terminal
 RT portion with rat identifies primary structural domains separated by
 RT hypervariable regions.";
 RL Biochemistry 24:2698-2704(1985).
 RN [14]
 RP SEQUENCE OF 1712-1739 FROM N.A.
 RX MEDLINE=87026578; PubMed=5021206;
 RA Sekiguchi K., Kios A.M., Kurechi K., Yoshitake S., Hakomori S.;
 RT "Human liver fibronectin complementary DNAs: identification of two
 RT different messenger RNAs possibly encoding the alpha and beta
 RT subunits of plasma fibronectin.";
 RL Biochemistry 25:4936-4941(1986).
 RN [15]
 RP SEQUENCE OF 1788-2386 FROM N.A. (ISOFORMS 4; 5 AND 6).
 RC TISSUE=Cartilage;
 RX MEDLINE=22126816; PubMed=12127832;
 RA Parker A.E., Boutell J., Carr A., Maciewicz R.A.;
 RT "Novel cartilage-specific splice variants of fibronectin.";
 RL Osteoarthritis Cartilage 10:528-534(2002).
 RN [16]
 RP SEQUENCE OF 32-290.
 RX MEDLINE=84032463; PubMed=6630202;
 RA Garcia-Pardo A., Pearlstein E., Frangione B.;
 RT "Primary structure of human plasma fibronectin. The 29,000-dalton
 RT NH2-terminal domain.";
 RL J. Biol. Chem. 258:12670-12674(1983).
 RN [17]
 RP SEQUENCE OF 309-608, AND COLLAGEN-BINDING.
 RX MEDLINE=87080265; PubMed=3024962;
 RA Owens R.J., Baralle F.E.;
 RT "Mapping the collagen-binding site of human fibronectin by expression
 RT in Escherichia coli.";
 RL EMBO J. 5:2825-2830(1986).
 RN [18]
 RP SULFATION.
 RX MEDLINE=86042625; PubMed=2413772;
 RA Liu M.C., Yu S.-S.Y. J., Redman C.M., Lipmann F.;
 RT "Tyrosine sulfation of proteins from the human hepatoma cell line
 RT HepG2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
 RN [19]
 RP O-GLYCOSYLATION OF THR-2064.
 RX MEDLINE=91190085; PubMed=2012601;

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RA  Tresselt T., McCarthy J. B., Calaycay J., Lee T.D., Legesse K.,
RA  Shively J.E., Pande H.;
RT  "Human plasma fibronectin. Demonstration of structural differences
RT  between the A- and B-chains in the III CS region.";
RL  Biochem. J. 274:731-738(1991).
RN  [20]
RP  PRINT-BINDING SITE.
RX  MEDLINE=93015879; Pubmed=1400330;
RA  Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K.,
RA  Argreaves W.S.;
RT  "Fibulin binds to itself and to the carboxyl-terminal heparin-binding
RT  region of fibronectin.";
RL  J. Biol. Chem. 267:20120-20125(1992).
RN  [21]
RP  CHARACTERIZATION OF FIBRIN-BINDING SITE 1.
RX  MEDLINE=95081153; Pubmed=7989369;
RA  Roetigano A., Williams M.J., Baron M., Campbell I.D., Gold L.I.;
RT  "Further characterization of the NH2-terminal fibrin-binding site on
RT  fibronectin.";
RL  J. Biol. Chem. 269:31938-31945(1994).
RN  [22]
RP  STRUCTURE BY NMR OF 1447-1540.
RX  MEDLINE=92162710; Pubmed=131102;
RA  Baron M., Main A.L., Driscoll P.C., Mardon H.J., Boyd J.,
RA  Campbell I.D.;
RT  "1H NMR assignment and secondary structure of the cell adhesion type
RT  III module of fibronectin.";
RL  Biochemistry 31:2068-2073(1992).
RN  [23]
RP  STRUCTURE BY NMR OF 1447-1540.
RX  MEDLINE=93046665; Pubmed=1423622;
RA  Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.;
RT  "The three-dimensional structure of the tenth type III module of
RT  fibronectin: an insight into RGD-mediated interactions.";
RL  Cell 71:671-678(1992).
RN  [24]
RP  STRUCTURE BY NMR OF 182-275.
RX  MEDLINE=94141923; Pubmed=8308892;
RA  Williams M.J., Phan I., Harvey T.S., Roetigano A., Gold L.I.,
RA  Campbell I.D.;
RT  "Solution structure of a pair of fibronectin type 1 modules with
RT  fibrin binding activity.";
RL  J. Mol. Biol. 235:1302-1311(1994).
RN  [25]
RP  STRUCTURE BY NMR OF 32-92.
RX  MEDLINE=96069779; Pubmed=7583666;
RA  Potts J.R., Phan I., Williams M.J., Campbell I.D.;
RT  "High-resolution structural studies of the factor XIIIa crosslinking
RT  site and the first type I module of fibronectin.";
RL  Nat. Struct. Biol. 2:946-950(1995).
RN  [26]
RP  STRUCTURE BY NMR OF 406-464.
RX  MEDLINE=96179558; Pubmed=9514732;
RA  Sticht H., Pickford A.R., Potts J.R., Campbell I.D.;
RT  "Solution structure of the glycosylated second type 2 module of
RT  fibronectin.";
RL  J. Mol. Biol. 276:177-187(1998).
RN  [27]
RP  STRUCTURE BY NMR OF EXTRA ED-B DOMAIN FROM ISOFORM 7.
RN  [28]
OY  1 KPSSPPE 8
DB  1939 KPSSPPE 1946

Query Match 79.5%; Score 35; DB 1; Length 2386;
Best Local Similarity 75.0%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 23
FIND_MOUSE STANDARD; PRT, 2477 AA.
ID FING_MOUSE
IC P11276; Q61567; Q61568; Q61569; Q64233; Q80U14;

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DT 01-JUL-1989 (Rel. 11, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Fibronectin precursor (FN).
 GN FN1.
 OS Mus musculus (Mouse).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE OF 1-920 FROM N.A.
 RC STRAIN=FVB/N-3; TISSUE=Breast tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hopsch S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshitoki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullah S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchéz A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schenck A., Schein J.E., Jones S.J.M., Matra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE OF 1-28 FROM N.A.
 RC TISSUE=Liver.
 RX MEDLINE=94131313; PubMed=8299972;
 RA Polly P., Nicholson R.C.;
 RT "Sequence of the mouse fibronectin-encoding gene promoter region.";
 RL Gene 137:353-354(1993).
 RN [3]
 RP SEQUENCE OF 562-834 FROM N.A.
 RC STRAIN=MNR1;
 RX MEDLINE=95403556; PubMed=7673336;
 RA Talts J.F., Weller A., Timpl R., Ekblom M., Ekblom P.;
 RT "Regulation of mesenchymal extracellular matrix protein synthesis by
 RT transforming growth factor-beta and glucocorticoids in tumor
 RT stroma.";
 RL J. Cell Sci. 108:2153-2162(1995).
 RN [4]
 RP SEQUENCE OF 899-2376 FROM N.A.
 RC Gorski G., Aros M., Norton P.;
 RX Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RL [5]
 RP SEQUENCE OF 2375-2477 FROM N.A.
 RX MEDLINE=8124987; PubMed=3124113;
 RA Blatti S.P., Foster D.N., Ranganathan G., Moses H.L., Getz M.J.;
 RT "Induction of fibronectin gene transcription and mRNA is a primary
 RT response to growth-factor stimulation of AKR-2B cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:1119-1123(1988).
 RN [6]
 RP SEQUENCE OF 2375-2477 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93011702; PubMed=1327855;
 RA Khadjian E.W., Salomon C., Leonard N., Tremblay S., Turlet H.;
 RT "Fibronectin gene expression in proliferating, quiescent, and SV40-
 RT infected mouse kidney cells.";
 RL Exp. Cell Res. 202:464-470(1992).
 RN [7]
 RP STRUCTURE BY NMR OF 1447-1630.
 RX MEDLINE=98202578; PubMed=9533887;
 RA Copie V., Tomita Y., Akiyama S.K., Aota S., Yamada K.M., Venable R.M.,
 RA Pastor R.W., Krueger S., Torchia D.A.;

RT "solution structure and dynamics of linked cell attachment modules of
 RT mouse fibronectin containing the RGD and synergy regions: comparison
 RT with the human fibronectin crystal structure.";
 RL J. Mol. Biol. 277:663-682(1998).
 RN [8]
 RP DOWN-REGULATION BY GLUCOCORTICOID.
 RX MEDLINE=21600963; PubMed=11737251;
 RA Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;
 RT "Glucocorticoids down-regulate the extracellular matrix proteins
 RT fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma.";
 RL Eur. J. Haematol. 67:176-184(2001).
 CC -1- FUNCTION: Fibronectin bind cell surfaces and various compounds
 CC including collagen, fibrin, heparin, DNA, and actin. Fibronectin
 CC are involved in cell adhesion, cell motility, opsonization, wound
 CC healing, and maintenance of cell shape.
 CC -1- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
 CC variants, connected by 2 disulfide bonds near the carboxyl ends;
 CC to a lesser extend homodimers. Interacts with PDN1 (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Comment=A number of isoforms are produced. Each of the "extra
 CC domain" and the connecting strand 3 are present in some forms of
 CC fibronectin and absent in others;
 CC Name=1;
 CC IsoId=P11276-1; Sequence=Displayed;
 CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
 CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
 CC forms), made by fibroblasts, epithelial and other cell types, is
 CC deposited as fibrils in the extracellular matrix.
 CC -1- INDUCTION: Glucocorticoids suppressed mRNA expression and protein
 CC synthesis.
 CC -1- PTM: Sulfated (By similarity).
 CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
 CC -1- SIMILARITY: Contains 17 fibronectin type III domains.
 CC -----
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 CC -----
 DR EMBL: BC051082; AAH51082.1; -.
 DR EMBL: Z22729; CA80422.1; -.
 DR EMBL: X82402; CA57796.1; -.
 DR EMBL: X93167; CA63654.1; -.
 DR EMBL: M8194; AAA37636.1; -.
 DR EMBL: S45680; AAB23491.1; -.
 DR PIR: A49173; AA9173.
 DR PIR: I48349; I48349.
 DR PDB: IMFN; 29-APR-98.
 DR PDB: 2MFN; 29-APR-98.
 DR MGD: MGI:95566; Fnl.
 DR GO: GO:0007155; P:cell adhesion; IDA.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR000083; Fibnctn1.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR000562; FN_Type_II.
 DR InterPro: IPR003962; FNIII subd.
 DR InterPro: IPR008924; MCR_alpha_beta_C.
 DR PRINTS: PRO0014; EWTYPER11.
 DR SMART: SM00058; FN1; 4.
 DR SMART: SM00060; FN3; 12.
 DR PROSITE: PS00022; EGF_1; 2.
 DR PROSITE: PS00023; FIBRONECTIN_2; 2.
 DR PROSITE: PS01253; FIBRONECTIN_1; 12.
 KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Phosphorylation;
 KW Sulfation; Cell adhesion; Repeat; Alternative splicing; Signal;

3d-structure. 1 32
 FT SIGNAL 2477
 FT CHAIN 53 273
 FT DOMAIN 308 608
 FT DNA_BIND 906 1171
 FT DOMAIN 1357 1630
 FT DOMAIN 1811 2081
 FT DOMAIN 2296 2427
 FT DOMAIN 51 36
 FT DOMAIN 96 140
 FT DOMAIN 140 185
 FT DOMAIN 185 230
 FT DOMAIN 230 272
 FT DOMAIN 306 343
 FT DOMAIN 345 404
 FT DOMAIN 404 469
 FT DOMAIN 468 516
 FT DOMAIN 516 559
 FT DOMAIN 559 602
 FT DOMAIN 609 706
 FT DOMAIN 707 808
 FT DOMAIN 809 903
 FT DOMAIN 904 994
 FT DOMAIN 995 1084
 FT DOMAIN 1085 1172
 FT DOMAIN 1173 1264
 FT DOMAIN 1265 1355
 FT DOMAIN 1356 1446
 FT DOMAIN 1447 1536
 FT DOMAIN 1537 1630
 FT DOMAIN 1631 1720
 FT DOMAIN 1721 1810
 FT DOMAIN 1811 1902
 FT DOMAIN 1903 1991
 FT DOMAIN 1992 2081
 FT DOMAIN 2082 2201
 FT DOMAIN 2202 2283
 FT DOMAIN 2294 2338
 FT DOMAIN 2339 2381
 FT DOMAIN 2383 2426
 FT SITE 1614 1616
 FT SITE 2181 2183
 FT DISULFID 53 79
 FT DISULFID 77 88
 FT DISULFID 98 126
 FT DISULFID 124 136
 FT DISULFID 142 170
 FT DISULFID 168 180
 FT DISULFID 187 216
 FT DISULFID 214 226
 FT DISULFID 232 261

Query Match 79.5%; Score 35; DB 1; Length 2477;
 Best Local Similarity 75.0%; Pred. No. 7e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
 Db 2029 KPSSPPE 2036

RESULT 24
 PINC_RAT STANDARD; PRT; 2477 AA.
 ID PINC_RAT
 AC P04937;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Fibronectin precursor (FN).
 GN FNI.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fischer; TISSUE=Liver;
 RX MEDLINE=8054951; PubMed=2445560;
 RA Schwarzbauer J.E., Patel R.S., Fonda D., Hynes R.O.;
 RT "Multiple sites of alternative splicing of the rat fibronectin gene transcript";
 RL EMBO J. 6:2573-2580(1987).
 RN [2]
 RP SEQUENCE OF 1-139 AND 2382-2477 FROM N.A.
 RC STRAIN=Fischer; TISSUE=Liver;
 RX MEDLINE=8054950; PubMed=3119323;
 RA Patel R.S., Odermatt E., Schwarzbauer J.E., Hynes R.O.;
 RT "Organization of the fibronectin gene provides evidence for exon shuffling during evolution";
 RL EMBO J. 6:2565-2572(1987).
 RN [3]
 RP SEQUENCE OF 1586-2477 FROM N.A.
 RX MEDLINE=84082067; PubMed=6317187;
 RA Schwarzbauer J.E., Tamkun J.W., Lemischka I.R., Hynes R.O.;
 RT "Three different fibronectin mRNAs arise by alternative splicing within the coding region.";
 RL Cell 35:421-431(1983).
 CC -1- FUNCTION: Fibronectins bind cell surfaces and various compounds including collagen, fibrin, heparin, DNA and actin. Fibronectins are involved in cell adhesion, cell motility, opsonization, wound healing, and maintenance of cell shape.
 CC -1- SUBUNIT: MOSTLY HETERODIMERS OR MULTIMERS OF ALTERNATIVELY SPLICED VARIANT, CONNECTED BY 2 DISULFIDE BONDS NEAR THE CARBOXYL ENDS; TO A LESSER EXTEND HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Each of the "extra domain" and the connecting strand 3 are present in some forms of fibronectin and absent in others;
 CC Name=1;
 CC IsoId=P04937-1; Sequence=displayed;
 CC Name=2; Synonyms=FNIII-13-1ess;
 CC IsoId=P04937-2; Sequence=VSP_003258;
 CC Name=3; Synonyms=Lambda-RLF4-5;
 CC IsoId=P04937-3; Sequence=VSP_003259;
 CC Name=4; Synonyms=Lambda-RLF6;
 CC IsoId=P04937-4; Sequence=VSP_003260;
 CC -1- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted by hepatocytes. Cellular FN (dimeric or cross-linked multimeric forms), made by fibroblasts, epithelial and other cell types, is deposited as fibrils in the extracellular matrix.
 CC -1- PTM: Sulfated (By similarity).
 CC -1- SIMILARITY: Contains 12 fibronectin type I domains.
 CC -1- SIMILARITY: Contains 2 fibronectin type II domains.
 CC -1- SIMILARITY: Contains 17 fibronectin type III domains.
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 CC -----
 DR EMBL; X15906; CAA34020.1; -;
 DR EMBL; L29191; AAA41166.1; -;
 DR EMBL; L00191; AAA41166.1; JOINED.
 DR EMBL; L29191; AAA41167.1; -;
 DR EMBL; L29191; AAA41167.1; JOINED.
 DR EMBL; L00191; AAA41168.1; -;
 DR EMBL; L00191; AAA41168.1; JOINED.
 DR EMBL; X05831; CAA29278.1; -;
 DR EMBL; X05832; CAA29279.1; -;
 DR EMBL; X05833; CAA29280.1; -;
 DR EMBL; X05834; CAA29281.1; -;

DR PIR; S14428; S14428.
 DR HSSP; P02751; 1FBR.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR000083; Fibnctnl.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR003962; FNII_subd.
 DR Pfam; PF00040; fn1; 12.
 DR Pfam; PF00040; fn2; 2.
 DR Pfam; PF00041; fn3; 17.
 DR PRINTS; PRO0013; ENTPEPIL.
 DR PRINTS; PRO0014; ENTPEPIL.
 DR ProDom; PD000995; FN_Type_II; 2.
 DR SMART; SM00058; FN1; 12.
 DR SMART; SM00059; FN2; 2.
 DR SMART; SM00060; FN3; 13.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS01253; FIBRONECTIN_1; 12.
 KW Glycoprotein; Plasma; Heparin-binding; Acute phase; Phosphorylation;
 KW Sulfation; Cell adhesion; Repeat; Alternative splicing; Signal.
 FT CHAIN 1 32
 FT DOMAIN 33 2477 FIBRONECTIN.
 FT 53 273 FIBRIN- AND HEPARIN-BINDING 1.
 FT 308 608 COLLAGEN-BINDING.
 FT 906 1171
 FT 1357 1630
 FT 1811 2081
 FT 2296 2427
 FT 51 91
 FT 96 139
 FT 140 183
 FT 185 229
 FT 230 274
 FT 306 345
 FT 345 404
 FT 405 469
 FT 468 511
 FT 516 558
 FT 559 602
 FT 609 706
 FT 707 808
 FT 809 903
 FT 904 994
 FT 995 1084
 FT 1085 1172
 FT 1173 1264
 FT 1265 1355
 FT 1356 1446
 FT 1447 1536
 FT 1537 1630
 FT 1631 1720
 FT 1721 1810
 FT 1811 1902
 FT 1903 1991
 FT 1992 2081
 FT 2082 2201
 FT 2202 2283
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 FT 77 88
 FT 98 126
 FT 126 136
 FT 136 142
 FT 142 170
 FT 170 180
 FT 180 216
 FT 216 226
 FT 226 261
 FT 261 232

FT DISULFID 259 271 BY SIMILARITY.
 FT DISULFID 308 335 BY SIMILARITY.
 FT DISULFID 333 342 BY SIMILARITY.
 FT DISULFID 360 386 BY SIMILARITY.
 FT DISULFID 374 401 BY SIMILARITY.
 FT DISULFID 420 446 BY SIMILARITY.
 FT DISULFID 434 461 BY SIMILARITY.
 FT DISULFID 470 498 BY SIMILARITY.
 FT DISULFID 496 508 BY SIMILARITY.
 FT DISULFID 518 545 BY SIMILARITY.
 FT DISULFID 543 555 BY SIMILARITY.
 FT DISULFID 561 589 BY SIMILARITY.
 FT DISULFID 587 599 BY SIMILARITY.
 FT DISULFID 2296 2325 BY SIMILARITY.
 FT DISULFID 2323 2335 BY SIMILARITY.
 FT DISULFID 2341 2368 BY SIMILARITY.
 FT DISULFID 2366 2378 BY SIMILARITY.
 FT DISULFID 2385 2409 BY SIMILARITY.
 FT DISULFID 2407 2423 BY SIMILARITY.
 FT DISULFID 2458 2458 INTERCHAIN (WITH C-2462).
 FT DISULFID 2462 2462 INTERCHAIN (WITH C-2458).
 FT MOD_RES 875 875 SULFATION (POTENTIAL).
 FT MOD_RES 880 880 SULFATION (POTENTIAL).
 FT MOD_RES 2392 2392 SULFATION (POTENTIAL).
 FT MOD_RES 2475 2475 PHOSPHORYLATION (BY SIMILARITY).
 FT CARBOHYD 430 430 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 528 528 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 876 876 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1006 1006 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1243 1243 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 1298 2198 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 2154 2154 O-LINKED (GALNAC. . .) (BY SIMILARITY).
 FT VARSPLIC 1720 1809 Missing (in isoform 2).
 FT VARSPLIC 2082 2106 Missing (in isoform 3).
 FT VARSPLIC 2082 2200 Missing (in isoform 4).
 FT VARSPLIC 2082 2200 Missing (in isoform 3).
 FT CONFLICT 2318 2318 G -> A (IN REF. 3).
 FT SEQUENCE 2477 AA; 272510 MW; B4391A472ECDEB5 CRC64;
 SQ SEQUENCE 2477 AA; 272510 MW; B4391A472ECDEB5 CRC64;
 Query Match 79.5%; Score 35; DB 1; Length 2477;
 Best Local Similarity 75.0%; Pred. No. 7e+02; Mismatches 0; Gaps 0;
 Matches 6; Conservative 0; Indels 2;
 Oy 1 KPSPPEE 8
 Db 2029 KPSPPEE 2036
 RESULT 25
 GBF3_ARATH STANDARD; PRT; 382 AA.
 AC P4276;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE G-box binding factor 3.
 GN GBF3 OR AT2G46270 OR T3P17.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA MEDLINE=96240020; PubMed=8672884;
 RA Lu G.H., Paul A.L., McCarty D.R., Perl R.J.;
 RT "transcription factor vcracty1: is GBF3 responsible for ABA-regulated
 expression of Arabidopsis Adh1";
 RL Plant Cell 8:847-857(1996).

RN [2] SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Macon T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Roming C.M., Xoo H.L.,
 RA Moffett K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umeyan L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creaey T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Niehan W.C., White O., Bisen J.A., Salzberg S.L., Frazer C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:761-768(1999).
 RN [3] SEQUENCE OF 59-382 FROM N.A.
 RP STRAIN=cv. Columbia; TISSUE=leaf, and stem;
 RX MEDLINE=92224864; PubMed=1373374;
 RA Schindler U., Menkens A.E., Beckmann H., Becker J.R., Cashmore A.R.;
 RT "Heterodimerization between light-regulated and ubiquitously
 RT expressed Arabidopsis GBR bZIP proteins.";
 RL EMBL J. 11:1261-1273(1992).
 CC -1- FUNCTION: Binds to the G-box motif (5'-CCACGTG-3') of the rbcS-1A
 CC gene promoter. G-box and G-box-like motifs are cis-acting elements
 CC defined in promoters of certain plant genes which are regulated by
 CC such diverse stimuli as light-induction or hormone control.
 CC -1- SUBUNIT: DNA-binding heterodimer.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: Present only in dark grown leaves and roots.
 CC -1- SIMILARITY: Belongs to the bZIP family.
 CC -----
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 CC -----
 CC EMBL, U17891; AAA0947.1; -
 CC EMBL, U17891; AAA0947.1; -
 CC EMBL, AC005397; AAC62879.1; -
 CC EMBL, X63896; CAA5358.1; -
 CC PIR; G84900; G84900.
 CC PIR; S20885; S20885.
 CC HSSP; P03069; IYSA.
 CC TRANSFAC; T01080; -
 CC InterPro; IPR004827; TF_bZIP.
 CC Pfam; PF00170; bZIP; 1.
 CC SMART; SM00338; BRLZ; 1.
 CC PROSITE; PS50217; BZIP; 1.
 CC PROSITE; PS00036; BZIP_BASIC; 1.
 CC KX Transcription regulation; DNA-binding; Nuclear protein.
 CC FT DOMAIN 8 121 PRO-RICH.
 CC FT DNA BIND 261 280 BASIC MOTIF.
 CC FT DOMAIN 287 315 LEUCINE-ZIPPER.
 CC FT CONFLICT 75 75 Y -> S (IN REF. 1).
 CC FT CONFLICT 366 366 L -> P (IN REF. 1).
 CC SQ SEQUENCE 382 AA; 41114 MW; 48B3176ZCDD977C CRC64;
 Query Match 77.3%; Score 34; DB 1; Length 382;
 Best Local Similarity 100.0%; Pred.No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC P34960;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Macrophage metalloelastase precursor (EC 3.4.24.65) (MME) (Matrix
 DE metalloproteinase-12) (MMP-12).
 GN MMP12 OR MME1 OR MME.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N.A., AND SEQUENCE OF 99-125.
 RP TISSUE=Macrophage;
 RX MEDLINE=92165826; PubMed=1537850;
 RA Shapiro S.D., Griffin G.L., Gilbert D.J., Jenkins N.A.,
 RA Copeland N.G., Welgus H.G., Senior R.M., Ley T.U.;
 RT "Molecular cloning, chromosomal localization, and bacterial
 RT expression of a murine macrophage metalloelastase.";
 RL J. Biol. Chem. 267:4664-4671(1992).
 CC -1- FUNCTION: May be involved in tissue injury and remodeling. Has
 CC significant elastolytic activity.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of soluble and insoluble elastin.
 CC Specific cleavages are also produced at 14-Ala-|-Leu-15 and 16-
 CC Tyr-|-Leu-17 in the B chain of insulin.
 CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to peptidase family M10A.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
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 CC -----
 CC EMBL, M62831; AAA39526.1; -
 CC PIR; A42401; A42401.
 CC HSSP; P03956; ICGL.
 CC MGD; MGI:97005; Mmp12.
 CC InterPro; IPR000585; Hemopexin.
 CC InterPro; IPR001818; Pept_M10A_M12B.
 CC InterPro; IPR006025; Pept_M_Zn_BS.
 CC InterPro; IPR006026; Peptidase_M.
 CC Pfam; PF00045; hemopexin; 4.
 CC Pfam; PF00413; Peptidase_M10; 1.
 CC Pfam; PF03933; Peptidase_M10_N; 1.
 CC PRINTS; PR00138; MATRXIN.
 CC SMART; SM00120; HX; 4.
 CC SMART; SM00235; Zmnc; 1.
 CC PROSITE; PS00024; HEMOPEXIN; 1.
 CC PROSITE; PS00142; ZINC_PROTEASE; 1.
 CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 CC KX Hydrolyase; Metalloproteinase; Glycoprotein; Calcium-binding;
 CC KW Metal-binding; Zinc; Zymogen; Extracellular matrix; Signal.
 CC FT SIGNAL 1 17 PROBABLE.
 CC FT PROPEP 18 98 ACTIVATION PEPTIDE.
 CC FT CHAIN 99 462 MACROPHAGE METALLOELASTASE.
 CC FT DOMAIN 272 462 CYSTEINE_SWITCH (BY SIMILARITY).
 CC FT SITE 117 117 CALCIUM 1 (BY SIMILARITY).
 CC FT METAL 151 151 CALCIUM 2 (BY SIMILARITY).
 CC FT METAL 161 161 ZINC 1 (BY SIMILARITY).
 CC FT METAL 163 163 ZINC 1 (BY SIMILARITY).
 CC FT METAL 168 168 CALCIUM 3 (BY SIMILARITY).
 CC FT METAL 169 169 CALCIUM 3 (VIA CARBOXYL OXYGEN) (BY
 CC SIMILARITY).
 CC FT METAL 171 171 CALCIUM 3 (VIA CARBOXYL OXYGEN) (BY
 CC SIMILARITY).
 CC FT METAL 173 173 CALCIUM 3 (VIA CARBOXYL OXYGEN) (BY

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FT METAL 176 176 SIMILARITY).
FT METAL 183 183 ZINC 1 (BY SIMILARITY).
FT METAL 187 187 CALCULUM 2 (VIA CARBONYL OXYGEN) (BY
FT METAL 189 189 SIMILARITY).
FT METAL 191 191 ZINC 1 (BY SIMILARITY).
FT METAL 192 192 CALCULUM 3 (BY SIMILARITY).
FT METAL 194 194 CALCULUM 1 (BY SIMILARITY).
FT METAL 211 211 CALCULUM 1 AND 3 (BY SIMILARITY).
FT ACT SITE 212 211 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT METAL 215 215 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT METAL 221 221 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT METAL 282 282 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT METAL 374 374 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT METAL 423 423 ZINC 2 (CATALYTIC) (BY SIMILARITY).
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 275 462 BY SIMILARITY.
SQ SEQUENCE 462 AA; 53841 MM; BB625906F1DBEDF CRC64;

Query Match 77.3%; Score 34; DB 1; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPP 6
DB 266 KPSSPP 271

RESULT 27
GAG_HV1C4 STANDARD; PRT; 499 AA.
ID_GAG_HV1C4
AC P05887;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polypeptide [contains: Core proteins P17, P24, P7, P1, P6].
GN GAG.
OS Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentiviridae; Lentivirus.
OX NCBI_TaxID=11687;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=67041461; Pubmed=3490666;
RA Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan A.,
RA Andersen P.R., Devare S.G.;
RT "Molecular cloning and primary nucleotide sequence analysis of a
RT distinct human immunodeficiency virus isolate reveal significant
RT divergence in its genomic sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- FUNCTION: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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DR EMBL: M13136; AAA44306.1; -.
DR PIR: A25523; FOVWH4.
DR HSP: P05888; 1AAF.
DR HIV: M13136; GAGSCD45.
DR InterPro: IPR000721; Gag_P24.
DR InterPro: IPR008916; Retrov_capsid_C.
DR InterPro: IPR008919; Retrov_capsid_N.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00540; Gag_P17; 1.
DR Pfam: PF00607; Gag_P24; 1.
DR Pfam: PF00098; Zf-CCHC; 2.
DR PRINTS: PR00939; C2HCZNFINGER.
DR SMART: SM00343; HIVMATRIX.
DR SMART: SM00343; Znf_C2HC; 2.
DR PROSITE: PS50158; Zf_CCHC; 2.
KW AIDS: Core protein; Polypeptide; Myristate; Phosphorylation;
KW Zinc-finger; Repeat; Lipoprotein.
FT INIT MET 0
FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
FT CHAIN 363 376 CORE PROTEIN P2.
FT CHAIN 377 431 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
FT CHAIN 432 447 CORE PROTEIN P1.
FT CHAIN 448 499 CORE PROTEIN P6.
FT ZN FING 389 406 CCHC-TYPE 1.
FT ZN FING 410 427 CCHC-TYPE 2.
FT LIPID 1 1 N-myristoyl glycine (in host) (By
FT similarity).
SQ SEQUENCE 499 AA; 55796 MM; 023CA76C9C6CF22AD CRC64;

Query Match 77.3%; Score 34; DB 1; Length 499;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
DB 453 EPTAPPE 460

RESULT 28
GAG_HV1H2 STANDARD; PRT; 499 AA.
ID_GAG_HV1H2
AC P04591;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polypeptide [contains: Core proteins P17, P24, P7, P1, P6].
GN GAG.
OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Lentiviridae; Lentivirus.
OX NCBI_TaxID=11706;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=6729196; Pubmed=3040055;
RA Retner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
RT virus."
RT AIDS Res. Hum. Retroviruses 3:57-69(1987).
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- FUNCTION: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
CC -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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DR EMBL; K03455; AAB50258.1; -
 DR PDB; 1B6J; 11-DEC-00.
 DR PDB; 1B6J; 21-APR-00.
 DR PDB; 1NCP; 31-OCT-93.
 DR PDB; 1TAM; 12-NOV-96.
 DR HIV; K03455; GAGSHXB2.
 DR InterPro; IPR000721; Gag_p24.
 DR InterPro; IPR008916; Retrov_capsid_C.
 DR InterPro; IPR008919; Retrov_capsid_N.
 DR InterPro; IPR000071; Retrov_p17.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00540; Gag_p17; 1.
 DR Pfam; PF00607; Gag_p24; 1.
 DR Pfam; PF00098; Zf_CCHC; 2.
 DR PRINTS; PR000939; C2HCZNFINGER.
 DR PRINTS; PR00234; HIVMATRIX.
 DR SMART; SM00343; Znf_CCHC; 2.
 DR PROSITE; PS50158; Zf_CCHC; 2.
 DR AIDS; Core protein; Polypeptide; Myristate; Phosphorylation;
 DR Zinc-finger; Repeat; 3D-structure; Lipoprotein.
 DR INIT MET 0
 FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
 FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
 FT CHAIN 363 376 CORE PROTEIN P2.
 FT CHAIN 377 431 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
 FT CHAIN 432 447 CORE PROTEIN P1.
 FT CHAIN 448 499 CORE PROTEIN P6.
 FT ZN_FING 389 406 CCHC-TYPE 1.
 FT ZN_FING 410 427 CCHC-TYPE 2.
 FT LIPID 1 N-myristoyl glycine (in host) (By similarity).
 SQ SEQUENCE 499 AA; 55798 MW; 774C384D6ACB108 CRC64;

Query Match 77.3%; Score 34; DB 1; Length 499;
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSPPEE 8
 Db 453 EPTAPPEE 460

RESULT 29
 GAG_HV1J3 STANDARD; PRT; 499 AA.
 AC P12434;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE GAG polyprotein [contains: Core proteins P17, P24, P2, P7, P1, P6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
 NCBI_TaxID=11694;
 OX (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89352108; PubMed=2669897;
 RA Komiyama N., Hattori N., Inoue J., Sakuma S., Kurimura T., Yoshida M.;
 RT "Nucleotide sequences of gag and env genes of a Japanese isolate of
 RT HIV-1 and their expression in bacteria."
 RL AIDS Res. Hum. Retroviruses 5:411-419(1989).
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
 CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT IMMEDIATELY
 CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
 CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
 CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

CC -1- P17: The p24 protein is phosphorylated.
 CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.
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DR EMBL; M21137; AAB03522.1; -
 DR HSSP; P05888; IAA.
 DR HIV; M21137; GAGSHXB3.
 DR InterPro; IPR000721; Gag_p24.
 DR InterPro; IPR008916; Retrov_capsid_C.
 DR InterPro; IPR008919; Retrov_capsid_N.
 DR InterPro; IPR000071; Retrov_p17.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00540; Gag_p17; 1.
 DR Pfam; PF00607; Gag_p24; 1.
 DR Pfam; PF00098; Zf_CCHC; 2.
 DR PRINTS; PR000939; C2HCZNFINGER.
 DR PRINTS; PR00234; HIVMATRIX.
 DR SMART; SM00343; Znf_CCHC; 2.
 DR PROSITE; PS50158; Zf_CCHC; 2.
 DR AIDS; Core protein; Polypeptide; Myristate; Phosphorylation;
 DR Zinc-finger; Repeat; Lipoprotein.
 DR INIT MET 0
 FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
 FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
 FT CHAIN 363 376 CORE PROTEIN P2.
 FT CHAIN 377 431 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
 FT CHAIN 432 447 CORE PROTEIN P1.
 FT CHAIN 448 499 CORE PROTEIN P6.
 FT ZN_FING 389 406 CCHC-TYPE 1.
 FT ZN_FING 410 427 CCHC-TYPE 2.
 FT LIPID 1 N-myristoyl glycine (in host) (By similarity).
 SQ SEQUENCE 499 AA; 55725 MW; 52E2812D4424ABE9 CRC64;

Query Match 77.3%; Score 34; DB 1; Length 499;
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPSPPEE 8
 Db 453 EPTAPPEE 460

RESULT 30
 GAG_HV1JW STANDARD; PRT; 499 AA.
 AC Q70622;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE GAG polyprotein [contains: Core proteins P17, P24, P2, P7, P1, P6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
 NCBI_TaxID=82834;
 OX (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95127297; PubMed=7826699;
 RA Raitz M.S. Jr., Hall J., Robert-Guroff M., Lautenberger J., Hahn B.M.,
 RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
 RT "Viral variability and serum antibody response in a laboratory worker
 RT infected with HIV type 1 (HIV type 1TIB)."
 RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM

OS Human immunodeficiency virus type 1 (RF/HAT isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
 OX NCBI_TaxID=11701;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S.,
 RA Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
 RA Wong-Staal F.;
 RL Submitted (XXX-1987) to the HIV data bank.
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
 CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
 CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
 CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
 CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
 CC -1- PTM: The p24 protein is phosphorylated.
 CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.
 CC -----
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 CC -----
 DR EMBL, M17451; AAA45052.1; --
 DR HSSP, P05888; 1AAF.
 DR HIV, M17451; GAGSRF.
 DR InterPro: IPR000721; Gag_p24.
 DR InterPro: IPR008916; Retrov_capsid_C.
 DR InterPro: IPR008919; Retrov_capsid_N.
 DR InterPro: IPR001878; Znf_CCHC.
 DR InterPro: IPR000071; Retrov_p17.
 DR Pfam: PF00540; Gag_p17; 1.
 DR Pfam: PF00607; Gag_p24; 1.
 DR Pfam: PF00098; Zf-CCHC; 2.
 DR PRINTS, PR00939; CCHCZNFINGER.
 DR PRINTS, PR00234; HIVMATRIX.
 DR SMART, SM00343; Znf_CCHC; 2.
 DR PROSITE, PSS0158; ZF_CCHC; 2.
 DR AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
 DR Zinc-finger; Repeat; Lipoprotein.
 DR INIT_MET 0
 FT CHAIN 1 131 BY SIMILARITY.
 FT CHAIN 1 362 CORE PROTEIN P17 (MATRIX PROTEIN).
 FT CHAIN 363 376 CORE PROTEIN P24 (CORE ANTIGEN).
 FT CHAIN 377 433 CORE PROTEIN P2.
 FT CHAIN 434 449 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
 FT CHAIN 450 500 CORE PROTEIN P1.
 FT ZN_FING 389 406 CORE PROTEIN P6.
 FT ZN_FING 410 427 CCHC-TYPE 1.
 FT ZN_FING 427 427 CCHC-TYPE 2.
 FT LIPID 1 N-myristoyl glycine (in host) (By
 FT LIPID 1 similarity).
 SQ SEQUENCE 500 AA; 55825 MW; 44AA0CB5CDAEFTB7B CRC64;
 QY Query Match 77.3%; Score 34; DB 1; Length 500;
 Db Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 RESULT 33
 ID _GAG_HVIA2 STANDARD; PRT; 501 AA.
 AC P03349;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE GAG polyprotein [contains: Core proteins P17, P24, P2, P7, P1, P6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
 OX NCBI_TaxID=11685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85090453; PubMed=2578227;
 RA Sanchez-Bescador R., Power M.D., Barr P.J., Steiner K.S.,
 RA Stempien M.W., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
 RA Levy J.A., Dina D., Luciw P.A.;
 RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
 RT (ARV-2).";
 RL Science 227:484-492 (1985).
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
 CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
 CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
 CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
 CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
 CC -1- PTM: The p24 protein is phosphorylated.
 CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.
 CC -----
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 DR EMBL, K02007; AAB5875.1; --
 DR PIR, A03947; FOVMZ.
 DR HSSP, P05888; 1AAF.
 DR HIV, K02007; GAGSRF2.
 DR InterPro: IPR000721; Gag_p24.
 DR InterPro: IPR008916; Retrov_capsid_C.
 DR InterPro: IPR008919; Retrov_capsid_N.
 DR InterPro: IPR000071; Retrov_p17.
 DR InterPro: IPR001878; Znf_CCHC.
 DR Pfam: PF00540; Gag_p17; 1.
 DR Pfam: PF00607; Gag_p24; 1.
 DR Pfam: PF00098; Zf-CCHC; 2.
 DR PRINTS, PR00939; CCHCZNFINGER.
 DR PRINTS, PR00234; HIVMATRIX.
 DR SMART, SM00343; Znf_CCHC; 2.
 DR PROSITE, PSS0158; ZF_CCHC; 2.
 DR AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
 DR Zinc-finger; Repeat; Lipoprotein.
 DR INIT_MET 0
 FT CHAIN 1 133 BY SIMILARITY.
 FT CHAIN 1 364 CORE PROTEIN P17 (MATRIX PROTEIN).
 FT CHAIN 365 378 CORE PROTEIN P24 (CORE ANTIGEN).
 FT CHAIN 379 433 CORE PROTEIN P2.
 FT CHAIN 434 449 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
 FT CHAIN 450 501 CORE PROTEIN P1.
 FT ZN_FING 391 408 CORE PROTEIN P6.
 FT ZN_FING 412 429 CCHC-TYPE 1.
 FT ZN_FING 429 429 CCHC-TYPE 2.
 FT LIPID 1 N-myristoyl glycine (in host) (By
 FT LIPID 1 similarity).
 SQ SEQUENCE 501 AA; 55935 MW; 8F36C928D5DBA45 CRC64;
 QY Query Match 77.3%; Score 34; DB 1; Length 501;
 Db Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 RESULT 34

GAG_HVLJR
ID GAG_HVLJR STANDARD; PRT; 503 AA.
AC P20873;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polypeptide [Contains: Core proteins P17, P24, P2, P7, P1, P6].
GN GAG.
OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11696;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.,
RL Submitted (DEC-1988) to the HIV data bank.
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
ASSEMBLY, BUDDING, MATURATION, AND INJECTION STAGES OF THE VIRAL
REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- PTM: The p24 protein is phosphorylated.
CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.

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EMBL; M38429; AAB03744.1; -.
DR PDB; 1KJ4; 06-MAR-02.
DR PDB; 1KJ7; 06-MAR-02.
DR HIV; M38429; GAGSURCSF.
DR InterPro; IPR000721; Gag_P24.
DR InterPro; IPR008915; Retrov_capsid_C.
DR InterPro; IPR008919; Retrov_capsid_N.
DR InterPro; IPR000071; Retrov_P17.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00540; Gag_P17; 1.
DR Pfam; PF00607; Gag_P24; 1.
DR Pfam; PF00098; zfc-CCHC; 2.
DR PRINTS; PR00939; C2HCZNFINGER.
DR PRINTS; PR00234; HIVMATRIX.
DR SMART; SM00343; Znf_CCHC; 2.
DR PROSITE; PS00158; ZF_CCHC; 2.
KW AIDS; Core protein; Polypeptide; Myristate; Phosphorylation;
KW zinc-finger; Repeat; 3D-structure; Lipoprotein.
FT INIT MET 0
FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
FT CHAIN 363 376 CORE PROTEIN P2.
FT CHAIN 377 431 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
FT CHAIN 432 447 CORE PROTEIN P1.
FT CHAIN 448 503 CORE PROTEIN P6.
FT ZN_P17 389 406 CCHC-TYPE 1.
FT ZN_P17 410 427 CCHC-TYPE 2.
FT LIPID 1 1 N-myristoyl glycine (in host) (By
similarity).
SQ SEQUENCE 503 AA; 56352 MM; F0B0471CC09B42BD CRC64;
Query Match 77.3%; Score 34; DB 1; Length 503;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 35
GAG_HVLJR
ID GAG_HVLJR STANDARD; PRT; 506 AA.
AC P05888;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polypeptide [Contains: Core proteins P17, P24, P2, P7, P1, P6].
GN GAG.
OS Human immunodeficiency virus type 1 (MN isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11696;
RN [1]
RP SEQUENCE, AND POST-TRANSLATIONAL MODIFICATIONS.
RX MEDLINE=92194415; PubMed=1548743;
RA Henderson L.E., Bowers M.A., Suther R.C. II, Serbryn S.A.,
RT Thomson D.G., Bees J.W., Jr., Arthur L.O., Bryant D.K., Fenselau C.;
RT "Gag proteins of the highly replicative MN strain of human
immunodeficiency virus type 1: posttranslational modifications,
proteolytic processes, and complete amino acid sequences.";
RT J. Virol. 66:1856-1865(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88219542; PubMed=3369091;
RA Garago C., Guo H.-G., Franchini G., Aldovini A., Collati E.,
RT Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
RT "Envelope sequences of two new United States HIV-1 isolates.";
RT Virology 164:531-536(1988).
RN [3]
RP STRUCTURE BY NMR OF 380-434.
RX MEDLINE=93278285; PubMed=1304355;
RA Summers M.F., Henderson L.E., Chance M.R., Bees J.W. Jr., South T.L.,
RA Blake P.R., Sagl I., Perez-Alvarado G., Sowder R.C. III, Hare D.R.,
RA Arthur L.O.;
RT "Nucleocapsid zinc fingers detected in retroviruses: EXAFS studies of
intact viruses and the solution-state structure of the nucleocapsid
protein from HIV-1.";
RT Protein Sci. 1:563-574(1992).
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
ASSEMBLY, BUDDING, MATURATION, AND INJECTION STAGES OF THE VIRAL
REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- PTM: The p24 protein is phosphorylated.
CC -1- MISCELLANEOUS: THE MN ISOLATE WAS TAKEN FROM A PEDIATRIC AIDS
PATIENT IN 1984.
CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.

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EMBL; M17449; AAA44853.1; -.
DR PIR; A38068; A38068.
DR PDB; 1A4F; 31-JAN-94.
DR HIV; M17449; GAGSMN.
DR InterPro; IPR000721; Gag_P24.
DR InterPro; IPR008915; Retrov_capsid_C.
DR InterPro; IPR008919; Retrov_capsid_N.
DR InterPro; IPR000071; Retrov_P17.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00540; Gag_P17; 1.
DR Pfam; PF00607; Gag_P24; 1.
DR Pfam; PF00098; zfc-CCHC; 2.
DR PRINTS; PR00939; C2HCZNFINGER.
DR PRINTS; PR00234; HIVMATRIX.

DR SMART; SM00343; ZNF C2HC; 2.
 DR PROSITE; PS0158; ZF CCHC; 2.
 KW AIDS; Core protein; Polypeptide; Myristate; Phosphorylation;
 KM Zinc-finger; 3D-structure; Repeat; Lipoprotein.
 FT CHAIN 1 134 CORE PROTEIN P17 (MATRIX ANTIGEN).
 FT INIT MET 0
 FT CHAIN 135 365 CORE PROTEIN P24 (CORE ANTIGEN).
 FT CHAIN 366 379 CORE PROTEIN P2.
 FT CHAIN 380 434 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
 FT CHAIN 435 450 CORE PROTEIN P1.
 FT CHAIN 451 506 CORE PROTEIN P6.
 FT ZN_FING 392 409 CCHC-TYPE 1.
 FT ZN_FING 413 430 CCHC-TYPE 2.
 FT LIPID 1 1 N-myristoyl glycine (in host).
 FT VARIANT 34 34 I -> V.
 FT VARIANT 45 45 R -> L OR S OR N.
 FT VARIANT 74 74 K -> E.
 FT VARIANT 92 92 K -> N (IN REF. 2).
 FT CONFLICT 17 17 Q -> E (IN REF. 2).
 FT CONFLICT 141 141 A -> V (IN REF. 2).
 FT CONFLICT 220 220 A -> T (IN REF. 2).
 FT CONFLICT 226 226 WM -> RT (IN REF. 2).
 FT CONFLICT 318 319 PG -> R (IN REF. 2).
 FT TURN 395 397
 FT HELIX 404 406
 FT TURN 416 418
 FT HELIX 425 427
 SQ SEQUENCE 506 AA; 56629 MW; AC6F3CEB691C4726 CRC64;
 Query Match 77.3%; Score 34; DB 1; Length 506;
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSPPEE 8
 Db 456 EPTAPPEE 463
 RESULT 36
 GAG_HV1B1 STANDARD; PRT; 511 AA.
 ID GAG_HV1B1
 AC P03347;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE GAG polyprotein [Contains: Core proteins P17, P24, P2, P7, P1, P6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8511123; PubMed=2578615;
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
 RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn B.A.,
 RA Baumsteiger K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
 RA Lautenberger J.A., Papas T.S., Ghayab J., Chang N.T., Gallo R.C.,
 RA Wong-Staal F.;
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 RL Nature 313:277-284(1985).
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
 CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
 CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
 CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
 CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
 CC -1- PTM: The p24 protein is phosphorylated.
 CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.
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 CC -----
 DR EMBL; M15654; AAA44201.1; -.
 DR PIR; A03945; FOVMH3.
 DR HSP; P05888; 1AIF.
 DR HIV; M15654; GAGSH102.
 DR InterPro; IPR000721; Gag_p24.
 DR InterPro; IPR008916; Retrov_capsid_C.
 DR InterPro; IPR008919; Retrov_capsid_N.
 DR InterPro; IPR000071; Retrovir_p17.
 DR InterPro; IPR001878; Znf CCHC.
 DR Pfam; PF00540; Gag_p17; 1.
 DR Pfam; PF00607; Gag_p24; 1.
 DR Pfam; PF00098; ZF-CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR PRINTS; PR00234; HIVMATRIX.
 DR SMART; SM00343; ZNF C2HC; 2.
 DR PROSITE; PS0158; ZF CCHC; 2.
 KW AIDS; Core protein; Polypeptide; Myristate; Phosphorylation;
 KM Zinc-finger; Repeat; Lipoprotein.
 FT INIT MET 0
 FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
 FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
 FT CHAIN 363 376 CORE PROTEIN P2.
 FT CHAIN 377 431 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
 FT CHAIN 432 447 CORE PROTEIN P1.
 FT CHAIN 448 511 CORE PROTEIN P6.
 FT ZN_FING 389 406 CCHC-TYPE 1.
 FT ZN_FING 410 427 CCHC-TYPE 2.
 FT LIPID 1 1 N-myristoyl glycine (in host) (By
 FT similarity).
 SQ SEQUENCE 511 AA; 57125 MW; 97C95188EB0D458 CRC64;
 Query Match 77.3%; Score 34; DB 1; Length 511;
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSPPEE 8
 Db 465 EPTAPPEE 472
 RESULT 37
 GAG_HV1B5 STANDARD; PRT; 511 AA.
 ID GAG_HV1B5
 AC P04593;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE GAG polyprotein [Contains: Core proteins P17, P24, P2, P7, P1, P6].
 GN GAG.
 OS Human immunodeficiency virus type 1 (BHS isolate) (HIV-1).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_Taxid=11682;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8511123; PubMed=2578615;
 RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
 RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn B.A.,
 RA Baumsteiger K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
 RA Lautenberger J.A., Papas T.S., Ghayab J., Chang N.T., Gallo R.C.,
 RA Wong-Staal F.;
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 RL Nature 313:277-284(1985).
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
 CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
 CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.


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CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- PFM: The p24 protein is phosphorylated.
CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.
-----
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-----
DR EMBL; K02012; AAA44652.1; -.
DR HSP; P05888; 1AAR.
DR HIV; K02012; GAGSBH5.
DR InterPro: IPR000721; Gag_p24.
DR InterPro: IPR008916; Retrov_capsid_C.
DR InterPro: IPR008919; Retrov_capsid_N.
DR InterPro: IPR000071; Retrovir_p17.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam; PF00540; Gag_p17; 1.
DR Pfam; PF00607; Gag_p24; 1.
DR Pfam; PF00098; Zf_CCHC; 2.
DR PRINTS; PR00939; C2HCZNFINGER.
DR PRINTS; PR00234; HIVMATRIX.
DR SMART; SM00343; ZNF_CCHC; 2.
DR PROSITE; PS50158; ZF_CCHC; 2.
DR AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
DR Zinc-finger; Repeat; Lipoprotein.
DR INIT_MET 0
DR CHAIN 0
FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
FT CHAIN 363 376 CORE PROTEIN P2.
FT CHAIN 377 431 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
FT CHAIN 432 447 CORE PROTEIN P1.
FT CHAIN 448 511 CORE PROTEIN P6.
FT CHAIN 511 511 CORE PROTEIN P6.
FT ZN_FING 389 406 CCHC-TYPE 1.
FT ZN_FING 410 427 CCHC-TYPE 2.
FT LIFID 1 1 N-myristoyl glycine (in host) (By similarity).
SQ SEQUENCE 511 AA; 57107 MW; EBAE72D3CBBE7A80 CRC64;

Query Match 77.3%; Score 34; DB 1; Length 511;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 465 EPTAPPE 472

RESULT 38
GAG_HV1BR STANDARD; PRT; 511 AA.
AC P03348;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polyprotein [Contains: Core proteins P17, P24, P2, P7, P1, P6].
GN GAG.
OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11686;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=5039333; Pubmed=2981635;
RT Wain-Hobson S., Sonigo P., Danos O., Cole S., Allison M.;
RL "Nucleotide sequence of the AIDS virus, LAV.";
RN [2]
RP REVISIONS TO 459-470.
RX MEDLINE=86245056; Pubmed=2424612;

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RA Allison M., Wain-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
RT of two isolates from African patients.";
RL Cell 46:63-74(1986).
-----
CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
CC -1- PFM: The p24 protein is phosphorylated.
CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.
-----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; K02013; AAB59747.1; -.
DR HSP; P05888; 1AAR.
DR HIV; K02013; GAGSBRU.
DR InterPro: IPR000721; Gag_p24.
DR InterPro: IPR008916; Retrov_capsid_C.
DR InterPro: IPR008919; Retrov_capsid_N.
DR InterPro: IPR000071; Retrovir_p17.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam; PF00540; Gag_p17; 1.
DR Pfam; PF00607; Gag_p24; 1.
DR Pfam; PF00098; Zf_CCHC; 2.
DR PRINTS; PR00939; C2HCZNFINGER.
DR PRINTS; PR00234; HIVMATRIX.
DR SMART; SM00343; ZNF_CCHC; 2.
DR PROSITE; PS50158; ZF_CCHC; 2.
DR AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
DR Zinc-finger; Repeat; Lipoprotein.
DR INIT_MET 0
DR CHAIN 0
FT CHAIN 1 131 CORE PROTEIN P17 (MATRIX PROTEIN).
FT CHAIN 132 362 CORE PROTEIN P24 (CORE ANTIGEN).
FT CHAIN 363 376 CORE PROTEIN P2.
FT CHAIN 377 431 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
FT CHAIN 432 447 CORE PROTEIN P1.
FT CHAIN 448 511 CORE PROTEIN P6.
FT CHAIN 511 511 CORE PROTEIN P6.
FT ZN_FING 389 406 CCHC-TYPE 1.
FT ZN_FING 410 427 CCHC-TYPE 2.
FT LIFID 1 1 N-myristoyl glycine (in host) (By similarity).
SQ SEQUENCE 511 AA; 57095 MW; 55972701A8434673 CRC64;

Query Match 77.3%; Score 34; DB 1; Length 511;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
Db 465 EPTAPPE 472

RESULT 39
GAG_HV1PV STANDARD; PRT; 511 AA.
AC P03350;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE GAG polyprotein [Contains: Core proteins P17, P24, P2, P7, P1, P6].
GN GAG.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_Taxid=11700;

```


[1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=6511157; PubMed=2982104;
 RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Laeky L.A.,
 RA Capon D.J.,
 RT "Nucleic acid structure and expression of the human
 RT AIDS/lymphadenopathy retrovirus.";
 RL Nature 313:450-458(1985).
 RN [2]
 RP REVISION.
 RA Muesing M.A.;
 RL Submitted (XXX-1987) to the HIV data bank.
 CC -1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
 CC ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
 CC REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
 CC MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
 CC RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
 CC GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
 CC BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
 CC -1- PTM: The p24 protein is phosphorylated.
 CC -1- SIMILARITY: Contains 2 CCHC-type zinc fingers.
 CC -----
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 CC -----
 CC EMBL; K02083; AAB59866.1; -
 CC EMBL; X01762; CAA25902.1; ALT_SEQ.
 CC PIR; A03948; FOVWVL.
 CC HSSP; P05888; 1AAP.
 CC HIV; K02083; GAGSPV2.
 CC InterPro; IPR000721; Gag_p24.
 CC InterPro; IPR008916; Retrov_capsid_C.
 CC InterPro; IPR008919; Retrov_capsid_N.
 CC InterPro; IPR000071; Retrov_p17.
 CC InterPro; IPR001878; Znf_CCHC.
 CC Pfam; PF00540; Gag_p17; 1.
 CC Pfam; PF00607; Gag_p24; 1.
 CC Pfam; PF00098; zf_CCHC; 2.
 CC PRINTS; PR00939; CCHCNFINGER.
 CC SMART; SM00343; HIVMATRIX.
 CC SMART; SM00343; Znf_CCHC; 2.
 CC PROSITE; PS50158; ZF_CCHC; 2.
 CC AIDS; Core protein; Polypeptide; Myristate; Phosphorylation;
 CC Zinc-finger; Repeat; Lipoprotein.
 CC KMW INIT MET 0
 CC FT CHAIN 1 131 BY SIMILARITY.
 CC FT CHAIN 132 362 CORE PROTEIN P17 (MATRIX PROTEIN).
 CC FT CHAIN 363 376 CORE PROTEIN P24 (CORE ANTIGEN).
 CC FT CHAIN 377 431 CORE PROTEIN P2.
 CC FT CHAIN 432 447 CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
 CC FT CHAIN 448 511 CORE PROTEIN P1.
 CC FT ZN_PING 389 406 CORE PROTEIN P6.
 CC FT ZN_PING 410 427 CCHC-TYPE 1.
 CC FT LIPID 1 1 N-myristoyl glycine (in host) (By
 CC similarity).
 CC SQ SEQUENCE 511 AA; 57139 MW; 397601C9403095F2 CRC64;

Query Match 77.3%; Score 34; DB 1; Length 511;
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSSPPEE 8
 DB 465 EPTAPPEE 472
 RESULT 40
 MIS_RAT

ID MIS_RAT STANDARD; PRT; 553 AA.
 AC P49000;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE MueLLerian inhibiting factor precursor (MIS) (Anti-mueLLerian hormone)
 DE (AMH) (MueLLerian inhibiting substance).
 GN AMH.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92241861; PubMed=1572639;
 RA Haeg C., Lee M.M., Tizard R., Wysk M., Demarinis J., Donahoe P.K.,
 RA Cate R.L.;
 RT "Isolation of the rat gene for MueLLerian inhibiting substance.";
 RL Genomics 12:665-669(1992).
 CC -1- FUNCTION: THIS GLYCOPROTEIN, PRODUCED BY THE SERTOLI CELLS OF THE
 CC TESTIS, CAUSES REGRESSION OF THE MUELLERIAN DUCT. IT ALSO IS ABLE
 CC TO INHIBIT THE GROWTH OF TUMORS DERIVED FROM TISSUES OF MUELLERIAN
 CC DUCT ORIGIN.
 CC -1- SUBUNIT: Homodimer; disulfide-linked.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; S98336; AAB22104.1; -
 CC PIR; A42499; A42499.
 CC InterPro; IPR006799; AMH_N.
 CC InterPro; IPR002400; GF_CysKnot.
 CC InterPro; IPR001839; TGFb.
 CC Pfam; PF04709; AMH_N; 1.
 CC Pfam; PF00019; TGF-beta; 1.
 CC PRINTS; PR00438; GFCYSKNOT.
 CC PRODOM; PD000357; TGFb; 1.
 CC SMART; SM00204; TGFb; 1.
 CC DR PROSITE; PS00250; TGF_BETA_1; 1.
 CC KMW Growth factor; Glycoprotein; Gonadal differentiation; Signal.
 CC FT SIGNAL 1 21 POTENTIAL.
 CC FT PROPEP 22 553 POTENTIAL.
 CC FT CHAIN 2 553 MUELLERIAN INHIBITING FACTOR.
 CC FT DISULFID 455 519 BY SIMILARITY.
 CC FT DISULFID 481 550 BY SIMILARITY.
 CC FT DISULFID 485 552 BY SIMILARITY.
 CC FT DISULFID 518 518 INTERCHAIN (BY SIMILARITY).
 CC FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 553 AA; 58888 MW; 75DAF3949A038A69 CRC64;

Query Match 77.3%; Score 34; DB 1; Length 553;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSSPPE 7
 DB 44 PSSPPE 49
 RESULT 41
 MIS_MOUSE
 ID MIS_MOUSE STANDARD; PRT; 555 AA.
 AC P27106;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Muellerian inhibiting factor precursor (MIS) (Anti-muellerian hormone)
 DE AMH (Muellerian inhibiting substance).
 GN AMH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Testis;
 RX MEDLINE=92146272; PubMed=1782869;
 RA Muensterberg A., Lovell-Badge R.;
 RT "Expression of the mouse anti-muellerian hormone gene suggests a role
 in both male and female sexual differentiation.";
 RL Development 113:613-624(1991).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RA Dresser D.W., Jamin S., Atkins C.J., Guerrier D.;
 RT "A GNP-like gene shares a bidirectional promoter with SAP62
 immediately upstream of AMH.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE OF 1-42 FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=96081226; PubMed=8541848;
 RA Dresser D.W., Hacker A., Lovell-Badge R., Guerrier D.;
 RT "The genes for a spliceosome protein (SAP62) and the anti-Muellerian
 hormone (AMH) are contiguous.";
 RL Hum. Mol. Genet. 4:1613-1618(1995).
 CC -1- FUNCTION: THIS GLYCOPROTEIN, PRODUCED BY THE SERTOLI CELLS OF THE
 TESTIS, CAUSES REGRESSION OF THE MUELLERIAN DUCT. IT ALSO IS ABLE
 TO INHIBIT THE GROWTH OF TUMORS DERIVED FROM TISSUES OF MUELLERIAN
 DUCT ORIGIN.
 CC -1- SUBUNIT: Homodimer; disulfide-linked.
 CC -1- TISSUE SPECIFICITY: SERTOLI CELLS OF TESTIS, AND TESTES
 JUST AFTER BIRTH, BUT ABSENT IN ADULT TESTES. IN FEMALE, AMH
 IS EXPRESSED AFTER BIRTH IN THE GRANULOSA CELLS OF FOLLICULAR
 MATURATION AND NOT ON THE AGE OF THE OVARY.
 CC -1- MISCELLANEOUS: Although it does not compete with EGF for receptor
 binding sites, MIS can inhibit the autophosphorylation of the EGF
 receptor in vitro.
 CC -1- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X63240; CAA44912.1; -;
 DR EMBL: X83733; CAC10450.1; -;
 DR PIR: S20100; S20100.
 DR MGD: MGI:88006; AMH.
 DR InterPro: IPR006799; AMH N.
 DR InterPro: IPR002400; GF_CysKnot.
 DR InterPro: IPR001839; TGFb.
 DR Pfam: PF04709; AMH_N; 1.
 DR Pfam: PF00019; TGF-beta; 1.
 DR PRINTS: PR00438; GFCYSKNOT.
 DR ProDom: PD000357; TGFb_1.
 DR SMART: SM00204; TGFb_1.
 DR PROSITE: PS00250; TGF_BETA_1; 1.
 KW Growth factor; Glycoprotein; Gonadal differentiation; Signal.
 FT SIGNAL 1 20
 FT PROPEP 21 ?
 FT CHAIN ? 555
 FT DISULFID 457 521
 FT DISULFID 483 552
 FT DISULFID 487 554
 FT BY SIMILARITY.
 FT BY SIMILARITY.

FT DISULFID 520 520 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 410 410 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 555 AA; 59778 MW; D6A3A20C50306E29 CRC64;
 Query Match 77.3%; Score 34; DB 1; Length 555;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 45 PSSPPE 50
 QY 2 PSSPPE 7
 DB 45 PSSPPE 50
 RESULT 42
 NR42 HUMAN STANDARD; PRT; 598 AA.
 AC P43354;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Orphan nuclear receptor NURR1 (immediate-early response protein NOT
 DE (transcriptionally inducible nuclear receptor).
 GN NR4A2 OR NURR1 OR T1NOR OR NOT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=95183071; PubMed=7877627;
 RA Mages H.W., Rilke O., Bravo R., Senger G., Kroczeck R.A.;
 RT "NOT, a human immediate-early response gene closely related to the
 RT steroid/thyroid hormone receptor NAK1/TR3.";
 RL Mol. Endocrinol. 8:1583-1591(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fibroblast;
 RX MEDLINE=99234104; PubMed=10216262;
 RA Ichinose H., Ohye T., Suzuki T., Sumi-Ichinose C., Nomura T.,
 RA Hagino Y., Nagatsu T.;
 RT "Molecular cloning of the human Nurrl gene: characterization of the
 RT human gene and cDNAs.";
 RL Gene 230:233-239(1999).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99234103; PubMed=10216261;
 RA Torii T., Kawarai T., Nakamura S., Kawakami H.;
 RT "Organization of the human orphan nuclear receptor Nurrl gene.";
 RL Gene 230:225-232(1999).
 [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=2388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein U.E., Jones S.J.M., Marra M.A.;

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RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences";
RT      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC      -1- FUNCTION: PROBABLE NUCLEAR RECEPTOR. MAY FUNCTION AS A GENERAL
CC      COACTIVATOR OF GENE TRANSCRIPTION. DETECTION OF THE PROTEIN IN
CC      THE BRAIN, INDICATES THAT IT IS NOT MANDATORILY ASSOCIATED WITH
CC      CELL CYCLE PROGRESSION.
CC      -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF CELL LINES OF T CELL,
CC      B CELL AND FIBROBLAST ORIGIN. STRONG EXPRESSION IN BRAIN TISSUE.
CC      -1- DEVELOPMENTAL STAGE: RAPIDLY AND ONLY VERY TRANSIENTLY EXPRESSED
CC      AFTER CELL ACTIVATION, DURING THE G0-G1 TRANSITION OF THE CELL
CC      CYCLE.
CC      -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR4
CC      subfamily.
CC      -----
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CC      -----
DR      EMBL; X75918; CA53518.1; -.
DR      EMBL; AB017586; BAA75666.1; -.
DR      EMBL; AB019433; BAA77328.1; -.
DR      EMBL; BC009288; AAO9288.1; -.
DR      PIR; A57040; A57040.
DR      HSSP; P19793; 2NLL.
DR      TRANSFAC; T02742; -.
DR      Gene; HGNC:7981; NR4A2.
DR      MIM; 601828; -.
DR      GO; GO:0005634; C:nucleus; TAS.
DR      GO; GO:0004879; F:ligand-dependent nuclear receptor activity; TAS.
DR      GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
DR      InterPro; IPR000536; Hormone_rec_1lg.
DR      InterPro; IPR001723; Stdhnm_receptor.
DR      InterPro; IPR008946; Str_ncl_receptor.
DR      InterPro; IPR001628; Znf_C4steroid.
DR      Pfam; PF00104; hormone_rec; 1.
DR      Pfam; PF00105; zf-C4; 1.
DR      PRINTS; PR00398; STRDHOMONER.
DR      PRINTS; PR00047; STROIDFINGER.
DR      ProDom; PD000035; Znf_C4steroid; 1.
DR      SMART; SM00430; HOL1; 1.
DR      SMART; SM00399; Znf_C4; 1.
DR      PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR      Receptor; Transcription regulation; DNA-binding; Nuclear protein;
DR      Zinc-finger.
KM      DOMAIN 80 138 GLN-RICH.
FT      DOMAIN 127 233 PRO-RICH.
FT      DOMAIN 263 328 NUCLEAR_RECEPTOR-TYPE.
FT      ZN_BIND 263 283 C4-TYPE.
FT      ZN_FING 299 323 C4-TYPE.
FT      ZN_FING 345 391 PRO-RICH.
FT      DOMAIN 409 459 LIGAND-BINDING (POTENTIAL).
SQ      SEQUENCE 598 AA; 66590 MW; 28D8199AC3BE211 CRC64;
Query Match 77.3%; Score 34; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 2; 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 KPSSPP 6
DB      123 KPSSPP 128
RESULT 43
NR42_MOUSE STANDARD; PRT; 598 AA.
AC      006219; 008690;
DT      01-JUN-1994 (Rel. 29, Created)

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DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Orphan nuclear receptor NURR1 (NUR-related factor 1).
GN      NR4A2 OR NURR1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10990;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RA      MEDLINE=93149122; Pubmed=1491694;
RA      Law S.W., Conneely O.M., Demayo F.J., O'Malley B.W.;
RT      Identification of a new brain-specific transcription factor, NURR1.;
RL      Mol. Endocrinol. 6:2129-2135(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SvJ;
RX      MEDLINE=97288523; Pubmed=9143501;
RA      Castillo S.O., Xiao O., Lyu M.S., Kozak C.A., Nikodem V.M.;
RT      Organization, sequence, chromosomal localization, and promoter
RT      identification of the mouse orphan nuclear receptor Nurrl gene.;
RL      Genomics 41:250-257(1997).
CC      -1- FUNCTION: PROBABLE NUCLEAR RECEPTOR THAT REGULATES GENE EXPRESSION
CC      IN BRAIN TISSUE.
CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=NURR1;
CC      IsoId=Q06219-1; Sequence=Displayed;
CC      Name=NURR1A;
CC      IsoId=Q06219-2; Sequence=VSP_003710, VSP_003711;
CC      IsoId=Q06219-2; Sequence=VSP_003710, VSP_003711;
CC      -1- TISSUE SPECIFICITY: Brain.
CC      -1- DEVELOPMENTAL STAGE: EXPRESSION BEGINS IN THE EMBRYO, INCREASES IN
CC      NEONATES AND DECREASES IN THE ADULT.
CC      -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR4
CC      subfamily.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; SS3744; AAB25138.1; -.
DR      EMBL; U86783; AAC53153.1; -.
DR      EMBL; U86783; AAC53154.1; -.
DR      PIR; A46225; A46225.
DR      HSSP; P19793; 2NLL.
DR      TRANSFAC; T04312; -.
DR      MGD; MGI:1352456; Nr4a2.
DR      GO; GO:0005634; C:nucleus; IDA.
DR      GO; GO:0007399; P:neurogenesis; IMP.
DR      InterPro; IPR000536; Hormone_rec_1lg.
DR      InterPro; IPR001723; Stdhnm_receptor.
DR      InterPro; IPR008946; Str_ncl_receptor.
DR      InterPro; IPR001628; Znf_C4steroid.
DR      Pfam; PF00104; hormone_rec; 1.
DR      Pfam; PF00105; zf-C4; 1.
DR      PRINTS; PR00398; STRDHOMONER.
DR      PRINTS; PR00047; STROIDFINGER.
DR      ProDom; PD000035; Znf_C4steroid; 1.
DR      SMART; SM00430; HOL1; 1.
DR      SMART; SM00399; Znf_C4; 1.
DR      PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR      Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KM      Zinc-finger; Alternative splicing.
FT      DOMAIN 80 138 GLN-RICH.
FT      DOMAIN 127 233 PRO-RICH.
FT      DOMAIN 263 328 NUCLEAR_RECEPTOR-TYPE.
FT      ZN_BIND 263 283 C4-TYPE.
FT      ZN_FING 299 323 C4-TYPE.

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FT ZN_FING 299 323 C4-TYPE.
FT DOMAIN 346 391 PRO-RICH.
FT DOMAIN 409 459 LIGAND-BINDING (POTENTIAL).
FT VARSPIC 455 455 S -> I (in isoform NURR1A).
FT VARSPIC 456 598 /FTId=VSP_003710.
SQ SEQUENCE 598 AA; 66592 MW; DIAC5EB2FFB8D366 CRC64;
Query Match 77.3%; Score 34; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KPSSPP 6
Db 123 KPSSPP 128

RESULT 44
NR42 RAT STANDARD; PRT; 598 AA.
ID NR42 RAT 007917; 035865;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Orphan nuclear receptor NURR1 (NUR-related factor 1) (Regenerating
DE liver nuclear receptor 1) (RNR-1) (SL-322) (Nuclear orphan receptor
DE HZF-3).
GN NR42 OR NURR1 OR RNR1 OR HZF-3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Hippocampus;
RX MEDLINE=94335560; PubMed=7914660;
RA de Ortiz S., Cannon M.M., Jamieson G.A.;
RT "Expression of nuclear hormone receptors within the rat hippocampus:
RT identification of novel orphan receptors."
RL Brain Res. Mol. Brain Res. 23:278-283 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93232045; PubMed=8473329;
RA Seearce L.M., Laz T.M., Hazel T.G., Lau L.F., Taub R.;
RT "NUR-1, a nuclear receptor in the NGFI-B/Nur77 family that is rapidly
RT induced in regenerating liver."
RL J. Biol. Chem. 268:885-886 (1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=97364974; PubMed=9221923;
RA Xing G.O., Zhang L.X., Zhang L., Heynen T., Li X.L., Smith M.A.,
RA Weiss S.R.B., Feldman A.N., DeCera-Wadleigh S., Chuang D.M.;
RT "Rat nurrl is prominently expressed in perirhinal cortex, and
RT differentially induced in the hippocampal dentate gyrus by
RT electroconvulsive vs. kindled seizures."
RL Brain Res. Mol. Brain Res. 47:251-261 (1997).
CC -1- FUNCTION: PROBABLE NUCLEAR RECEPTOR. MAY CONFER LIVER-SPECIFIC
CC REGULATION OF DELAYED-EARLY GENES INDUCED LATER IN THE G1 PHASE
CC OF REGENERATION ALONG WITH HMR.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: NOT EXPRESSED IN QUIESCENT LIVER BUT IS
CC RAPIDLY INDUCED FOLLOWING PARTIAL HEPATECTOMY AND IS SPECIFIC TO
CC HEPATIC GROWTH AS IT IS NOT INDUCED IN OTHER MITOGEN-TREATED
CC CELLS. EXPRESSED AT VERY LOW LEVELS IN THE LUNG, SPLEEN AND
CC STOMACH AND AT HIGH LEVELS IN THE BRAIN.
CC -1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR4
CC subfamily.
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CC -----
DR EMBL; U01146; AAC52143.1; -
DR EMBL; L08595; AAA42058.1; -
DR EMBL; U72345; AAC5315.1; -
DR PIR; I84692; I84692.
DR HSSP; P19793; ZML.
DR TRANSPAC; T04743; -
DR InterPro; IPR000536; Hormone_rec_1g.
DR InterPro; IPR001723; Sdrhnm_receptor.
DR InterPro; IPR008946; Str_ncl_receptor.
DR InterPro; IPR001628; ZnF_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00396; STRDHORMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR Prodom; PD000035; ZnF_C4steroid; 1.
DR SMART; SM00430; HOL1.1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KM Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KM Zinc-finger.
FT DOMAIN 80 138 GLN-RICH.
FT DOMAIN 127 233 PRO-RICH.
FT DNA_BIND 263 328 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 263 283 C4-TYPE.
FT ZN_FING 299 323 C4-TYPE.
FT DOMAIN 346 391 PRO-RICH.
FT DOMAIN 409 459 LIGAND-BINDING (POTENTIAL).
FT CONFLICT 182 182 R -> A (IN REF. 2).
FT CONFLICT 182 182 R -> P (IN REF. 3).
FT CONFLICT 250 250 S -> P (IN REF. 2).
FT CONFLICT 252 252 S -> A (IN REF. 1).
FT CONFLICT 362 362 V -> G (IN REF. 2).
FT CONFLICT 364 371 LISALVRA -> DOCPROT (IN REF. 2).
FT CONFLICT 434 434 D -> S (IN REF. 2).
SQ SEQUENCE 598 AA; 66621 MW; 0A54ED59FB70DEA8 CRC64;
Query Match 77.3%; Score 34; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KPSSPP 6
Db 123 KPSSPP 128

RESULT 45
Y013 SCHPO STANDARD; PRT; 615 AA.
ID Y013 SCHPO 013681;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C737.03c in chromosome III.
GN SPCC737.03c.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxId=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Baaham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

```

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentes S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Honnery T., Howarth S., Huckle E.J., Hunt S., Jagals K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., O'Neill C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbhnowlath E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodard J., Volcaert G., Aert R., Robben J., Grympey B.,
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabell C., Fuchs M., Fritsch C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Manbuit R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Gallbert F., Aves S.U., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foreburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Uesery D., Barrell B.G., Nurse P.,
 RA "The genome sequence of *Schizosaccharomyces pombe*."
 RL Nature 415:871-880(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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 CC
 CC EMBL: AL031546; CAA20860.1; -.
 DR PIR: T41576; T41576.
 DR GeneDB: Spombe; SPCC737.03c; -.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 192 212 POTENTIAL.
 FT TRANSMEM 247 267 POTENTIAL.
 FT TRANSMEM 323 343 POTENTIAL.
 FT TRANSMEM 563 583 POTENTIAL.
 FT TRANSMEM 586 606 POTENTIAL.
 FT DOMAIN 88 91 POLY-SER.
 SQ SEQUENCE 615 AA; 70433 MW; DSCA85894410064E CRC64;
 Query Match 77.3%; Score 34; DB 1; Length 615;
 Best Local Similarity 85.7%; Pred. No. 2.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KPSSPPE 7
 DB 344 KPSSPPE 350
 RESULT 46
 ID CN4A_HUMAN STANDARD; PRT; 886 AA.
 AC P27815; O75522; O76092; Q16255; Q16691; Q8W003;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE CAMP-specific 3',5'-cyclic phosphodiesterase 4A (EC 3.1.4.17)
 DE (DPDB2) (PDB46).
 GN PD34A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=94019330; PubMed=8413254;
 RA Bolger G., Michael T., Martins T., St John T., Steiner B.,
 RA Rodgers L., Riggs M., Wigler M., Ferguson K.,

RT "A family of human phosphodiesterases homologous to the dunc
 RT learning and memory gene product of *Drosophila melanogaster* are
 RT potential targets for antidepressant drugs."
 RL Mol. Cell. Biol. 13:6558-6571(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
 RC TISSUE=Brain;
 RX MEDLINE=98343959; PubMed=9677330;
 RA Sullivan M., Rana G., Begg F., Gordon L., Olsen A.S., Houslay M.D.;
 RT "Identification and characterization of the human homologue of the
 RT short PD34A cAMP-specific phosphodiesterase RDI (PD34A) by analysis
 RT of the human HSP34A gene locus located at chromosome 19p13.2."
 RL Biochem. J. 333:693-703(1998).
 RN [3]
 RP SEQUENCE OF 112-886 FROM N.A.
 RC TISSUE=Monocytes;
 RX MEDLINE=90258854; PubMed=2160582;
 RA Livi G.P., Kmetz P., McHale M.M., Cieplinski L.B., Sathe G.M.,
 RA Taylor D.P., Davis R.L., Torphy T.J., Balcarak J.M.;
 RT "Cloning and expression of cDNA for a human low-Km, rolipram-sensitive
 RT cyclic AMP phosphodiesterase."
 RL Mol. Cell. Biol. 10:2678-2686(1990).
 RN [4]
 RP REVISIONS TO REF. 3.
 RA McLaughlin M.M.;
 RL Submitted (JAN-1991) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 5).
 RX MEDLINE=95290008; PubMed=7772058;
 RA Horton Y.M., Sullivan M., Houslay M.D.;
 RT "Molecular cloning of a novel splice variant of human type IVA
 RT (PDE-IVA) cyclic AMP phosphodiesterase and localization of the gene
 RT to the p13.2-q12 region of human chromosome 19."
 RL Biochem. J. 308:683-691(1995).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=95194817; PubMed=7888306;
 RA Sullivan M., Egerton M., Shakur Y., Margardsen A., Houslay M.D.;
 RT "Molecular cloning and expression, in both COS-1 cells and S.
 RT cerevisiae, of a human cytosolic type-IVA, cyclic AMP specific
 RT phosphodiesterase (hPDE-IVA-h6.1)."
 RL Cell. Signal. 6:793-812(1994).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=Brain;
 RX MEDLINE=2388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton W., Soares M.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skaleka U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
 CC adenosine 5'-phosphate.
 CC -1- ENZYME REGULATION: Inhibited by rolipram.
 CC -1- PATHWAY: Cyclic nucleotide metabolism.
 CC -1- SUBCELLULAR LOCATION: Isoform 4 has propensity for association
 CC with membranes.
 CC -1- ALTERNATIVE PRODUCTS:

[illegible]

FT					SVTSEAHADLIYTPPAQVLASIRVSRNSFLTNTVPVS NKXS -> MCPPTTV (in isoform 3).
FT					/FtId=VSP_004557.
FT	VARSPLIC	1	261		METPVTSSERSLSLSTLPREGQAATLKPPPOHLMROQRPTPI RIORGRYSDSAERIEREROHRPIERDANDOTSREBELRTT
FT					RMSWPSFFHGITGTSGGAGGSRRFRFAENGPTPTS PERSPL
FT					DSEQASPGLVIHAGAATAOGRESFLYRSDSYDMSPKTRSN
FT					NKSVESEAHDLIYTTPAQQVLASIRSRSNPSLLTNVPVS
FT					NKRSLPGGPVVCAATLSEERTCOOLARETBELDWCKEQLB
FT					TMOYRVSRVSEMASHKFPRMLNRLETHISEMRSNGVOXEVJ
FT					LSTEFDIKONGVEIAPSPFMKEKOQAOPRPBPSCQPPEPVPH
FT					SOPSOLTGKLKMHSNLINNSNIIPRGVTDOEBELLAQ -> MVLPSDOGFKLGIVLOQGEPEPYRLTLTGRLRHQ (in isoform 5)
FT					/FtId=WSP_004559. GFIDLYHPMPMETW -> QARIGDGRAQGCFY (in isoform 5).
FT	VARSPLIC	644	657		/FtId=WSP_004560. Missing (in isoform 5).
FT					-> A (in Ref. 1, 2, 6, AMB33798 AND 7). E = >>
FT	VARSPLIC	658	886		E = >>
FT	CONFLICT	736	736		E = >>
SO	SEQUENCE	886 AA;	98201 MW;	483BDPFGBAB9756CA CRC64,	
	Query Match		77.3%;	Score 34;	DB 1; Length 886;
	Best Local Similarity		85.7%;	Pred. No. 3.4e+02;	
Matches	6;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
Oy	2 PSSPPEE 8				
Db	687 PSPPPPEE 693				
	RESULT 47				
ID	_RSC1_YEAST	STANDARD;	PRT;	928 AA.	
AC	P53236;				
DT	01-OCT-1996	(Rel. 34, Created)			
DR	01-OCT-1996	(Rel. 34, Last sequence update)			
DI	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Chromatin structure remodeling complex protein Rsc1.				
GN	RSC1 OR YGR056W.				
OS	Saccharomyces cerevisiae (Baker's yeast).				
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;				
NCBI_OX	[Taxid=4932;				
NP	SEQUENCE FROM N.A.				
RA	Enrian K.D., Rose M., Koetter P., Roehner A., Sehmsam I.,				
RA	Hempel S.;				
RL	Submitted (May-1996) to the EMBL/GenBank/DDBJ databases.				
CC	- FUNCTION: Component of the RSC chromatin remodeling complex. RSC				
CC	is responsible for the transfer of a histone octamer from a				
CC	nucleosome core particle to naked DNA.				
CC	- SUBUNIT: Rec is composed of 15 subunits; among which ARP7, ARP9,				
CC	RSC1, RSC2, RSC4, RSC6, RSC8, SPH1 and STL1.				
CC	- SIMILARITY: Contains 1 BAH domain.				
CC	- SIMILARITY: Contains 2 bromodomains.				
CC	-----				
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CC -----

DR EMBL, 272841; CA97057.1; -.

DR PIR, S643501; S64350.

DR HSSP, Q92831; 1B91.

DR GenOnline, 141368; -.

DR SGD, S0003288; RSC1.

DR GO, GO:0005679; C:nucleosome remodeling complex; IPL.

DR GO, GO:0006338; P:chromatin modeling; IDA.

DR InterPro, IPR001025; BAH.

DR InterPro, IPR001487; Bromodomain.

DR Pfam, PF01426; BAH; 1.

DR Pfam, PF00439; bromodomain; 2.

DR PRINTS, PRO0503; BROMODOMAIN.

DR SMART, SM00439; BAH; 1.

DR SMART, SM00297; BROMO; 2.

DR PROSITE, PS00633; BROMODOMAIN 1; 1.

DR PROSITE, PS00633; BROMODOMAIN 2; 2.

KW Chromatin regulator; Nuclear Protein; Bromodomain; Repeat.

FT DOMAIN 27 95 BROMODOMAIN 1.

FT DOMAIN 235 325 BROMODOMAIN 2.

SEQUENCE 928 AA; 106669 MW; EFP80922FC08EC27 CRC64;

Query Match 77.3%; Score 34; DB 1; Length 928;

Best local Similarity 62.5%; Pred. No. 3.6e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSSPBB 8

Db 575 RPMDPBB 582

RESULT 48

G2D1 HUMAN STANDARD; PRT; 959 AA.

AC Q9UHL9; O95444; O9UHC4; O9U91; 959 AA.

AD Q9UHL9; O95444; O9UHC4; O9U91; 959 AA.

DT 28-FEB-2003 (Rel. 41; Created)

DT 28-FEB-2003 (Rel. 41; Last sequence update)

DT 10-OCT-2003 (Rel. 42; Last annotation update)

DE General transcription factor II-I repeat domain-containing protein 1 (Muscle TFIID repeat domain-containing protein 1) (General transcription factor IIT) (Slow-muscle-fiber enhancer binding protein) (USE BI binding protein)

DE (MusTRD/BBR) (Williams-Beuren syndrome chromosome region 11 protein).

GN GF2LRD1 OR MUSTRD1 OR GF13 OR CREAM1 OR RBAF2 OR WBSCR11 OR WBSCR12.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Muscle;

RX MEDLINE=98449952; PubMed=9774679;

RA O'Mahoney J.V., Guven K.L., Lin J., Joya J.E., Robinson C.S., Wade R.P., Hardeman E.C.;

RT "Identification of a novel slow-muscle-fiber enhancer binding protein, MUSTRD1.";

RT Mol. Cell. Biol. 18:6641-6652(1998).

RL [2]

RN SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Colon carcinoma;

RX MEDLINE=99216421; PubMed=10198167;

RA Osborne L.R., Campbell T., Daradich A., Scherer S.W., Tsui L.-C.;

RT "Identification of a putative transcription factor gene (WBSCR11) that is commonly deleted in Williams-Beuren syndrome.";

RL Genomics 57:279-284(1999).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Fetal brain;

RX MEDLINE=20037629; PubMed=10573005;

RA Tassebejji M., Carette M., Wilmet C., Donnai D., Read A.P., Metcalfe K.;

RT "A transcription factor involved in skeletal muscle gene expression is deleted in patients with Williams syndrome.";

RL Eur. J. Hum. Genet. 7:737-747(1999).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=20044629; PubMed=10575229;

RA Franke Y., Peoples R.J., Francke U.;

RT "Identification of GF2LRD1, a putative transcription factor within the Williams-Beuren syndrome deletion at 7q11.23.";

RL Cytogenet. Cell Genet. 86:236-304(1999).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 1), INTERACTION WITH RB1, AND MUTAGENESIS.

RC TISSUE=Cervical carcinoma, Fetal spleen, and Placenta;

RX MEDLINE=20115113; PubMed=10642537;

RA Yan X., Zhao X., Qian M., Guo N., Gong X., Zhu X.;

RT "Characterization and gene structure of a novel retinoblastoma-protein-associated protein similar to the transcription regulator TFIID-1.";

RL Biochem. J. 345:749-757(2000).

RL [6]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Dermis;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.P., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J., Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield A.S.N., Krzywicki M.I., Skalska U., Smalins D.E., Scherf A., Schein J.E., Jones S.J.M., Maira M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [7]

RP FUNCTION.

RX MEDLINE=21332325; PubMed=11438732;

RA Tussie-Luna M.I., Bayarsaiban D., Ruddle F.H., Roy A.L.;

RT "Repression of TFIID-dependent transcription by nuclear exclusion.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:7789-7794(2001).

CC -1- FUNCTION: May be a transcription regulator involved in cell-cycle progression and skeletal muscle differentiation. May repress GF2LR transcriptional functions, by preventing its nuclear residency, or by inhibiting its transcriptional activation. May contribute to slow-twitch fiber type specificity during myogenesis and in regenerating muscles. Binds tropomyosin I slow-muscle fiber enhancer (USE BI). Binds specifically and with high affinity to the ERF sequences derived from the early enhancer of HOXB8 (By similarity).

CC -1- SUBUNIT: Interacts with the retinoblastoma protein (RB1) via its C-terminus.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q9UHL9-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q9UHL9-2; Sequence=VSP_003873;

CC -1- TISSUE SPECIFICITY: Highly expressed in adult skeletal muscle, heart, fibroblast, bone and fetal tissues. Expressed at lower levels in all other tissues tested.

CC -1- DEVELOPMENTAL STAGE: Highly expressed in developing and regenerating muscles, at the time of myofiber diversification.

CC -1- DOMAIN: The N-terminal half may have an activating activity.

```

CC -1- DISEASE: Haploinsufficiency of GTF2IRD1 may be the cause of
CC certain cardiovascular and musculo-skeletal abnormalities observed
CC in Williams-Beuren syndrome (WBS), a rare developmental disorder.
CC It is a contiguous gene deletion syndrome involving genes from
CC chromosome band 7p11.23
CC -1- SIMILARITY: BELONGS TO THE TFIID-1 FAMILY.
CC -1- SIMILARITY: Contains 5 GTF2I-like repeats.
CC -----
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CC -----
DR EMBL: AF118270; AAD14687.2; -
DR EMBL: AF104923; AAD27668.1; -
DR EMBL: AF151354; AAF19786.1; -
DR EMBL: AF156489; AAF17358.1; -
DR EMBL: AF089107; AAF21796.1; -
DR EMBL: BC018136; AAF18136.1; -
DR Gene: HGNC:4661; GTF2IRD1.
DR MIM: 604318; -
DR MIM: 194050; -
DR GO: GO:0005634; C:nucleus; NAS.
DR GO: GO:0003705; F:RNA polymerase II transcription factor acti...; NAS.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
DR InterPro: IPR004212; GTF2I.
DR Pfam: PF02946; GTF2I; 5.
DR Transcription regulation; Developmental protein; DNA-binding;
DR Nuclear protein; Repeat; Alternative splicing; Polymorphism;
DR Williams-Beuren syndrome.
DR REPEAT 128 203 GTF2I 1.
DR REPEAT 351 426 GTF2I 2.
DR REPEAT 565 640 GTF2I 3.
DR REPEAT 705 780 GTF2I 4.
DR REPEAT 802 877 GTF2I 5.
DR DOMAIN 898 905 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
DR DOMAIN 906 930 SER-RICH.
DR VARSPLIC 656 670 Missing (in isoform 2).
DR VARIANT 652 652 /FTId=VSP_003873.
DR M -> V (in dSNP:2301895).
DR MUTAGEN 898 959 /FTId=VAR_013446.
DR CONFLICT 111 111 MISSING: CYTOPLASMIC LOCALIZATION.
DR CONFLICT 378 378 G -> S (IN REF. 1 AND 2).
DR SEQUENCE 959 AA; 106057 MW; 7DA3097879701540 CRC64;
SQ
Query Match 77.3%; Score 34; DB 1; Length 959;
Best Local Similarity 62.5%; Pred. No. 3.7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSSPPE 8
DB 445 EPASPED 452

```

```

RP DEVELOPMENTAL STAGE, AND INTERACTION WITH SRF.
RC STRAIN=C57BL/6;
RX MEDLINE=22317395; PubMed=12397177;
RA Wang D.-Z., Li S., Hockemeyer D., Sutherland L., Wang Z., Schratz G.,
RA Richardson J.A., Nordheim A., Olson E.N.;
RT "Potentiation of serum response factor activity by a family of
RT myocardin-related transcription factors."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14855-14860(2002).
CC -1- FUNCTION: Poor transcriptional factor which uses the canonical
CC single or multiple CARG boxes DNA sequence. Acts as a cofactor of
CC serum response factor (SRF) with the potential to modulate SRF
CC target genes.
CC -1- SUBUNIT: Interacts with SRF.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- TISSUE SPECIFICITY: Widely expressed. High expression in heart,
CC brain and testis. Lower expression in lung, liver and kidney.
CC -1- DEVELOPMENTAL STAGE: Detected throughout the embryo at 10.5 dpc.
CC High expression in epithelial cells of the lung, kidney, bladder,
CC colon, testis, in the smooth muscle of the colon and small
CC intestines, and in the mesenchymal cells adjacent to the olfactory
CC epithelium at 15.5 dpc.
CC -1- DOMAIN: The N-terminal region is required for nuclear localization
CC and the C-terminal region mediates transcriptional activity (By
CC similarity). Contains 3 RPEL repeats.
CC -1- SIMILARITY: Contains 1 SAP domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF332598; AAN33042.1; -
DR InterPro: IPR004018; RPEL_repeat.
DR InterPro: IPR003034; SAP.
DR Pfam: PF02755; RPEL; 3.
DR Pfam: PF02037; SAP; 1.
DR SMART: SM00707; RPEL; 3.
DR SMART: SM00513; SAP; 1.
DR PROSITE: PS0800; SAP; 1.
DR Transcription regulation; Nuclear protein; Coiled coil; Repeat.
DR REPEAT 40 65 RPEL 1.
DR REPEAT 84 109 RPEL 2.
DR REPEAT 128 153 RPEL 3.
DR DOMAIN 320 346 GLN-RICH.
DR DOMAIN 383 417 SAP.
DR DOMAIN 539 594 COILED COIL (POTENTIAL).
DR DOMAIN 665 806 GLN-RICH.
DR SEQUENCE 1080 AA; 117546 MW; 1781D8EF24517DAC CRC64;
SQ
Query Match 77.3%; Score 34; DB 1; Length 1080;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSSP 6
DB 836 KPSSP 841

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RESULT 49
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ID MRTB_MOUSE
AC P59759;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myocardin-related transcription factor B (MRTF-B).
GN MRTFB.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A., CHARACTERIZATION, FUNCTION, TISSUE SPECIFICITY,

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RESULT 50
MRTB_HUMAN STANDARD; PRT; 1088 AA.
ID MRTB_HUMAN
AC Q9ULH7; Q86W2; Q8N226;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myocardin-related transcription factor B (MRTF-B).
GN MRTFB OR KIAA1243.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 CC [1] TaxID=9606;
 CC SEQUENCE FROM N.A. (ISOFORM 3).
 CC TISSUE=Thymus;
 CC Ohtsuka M., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
 CC Arita M., Musashino K., Yuki H., Hara H., Sugiyama T., Irie R.,
 CC Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
 CC Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 CC Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,
 CC "NEO human cDNA sequencing project."
 CC Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 CC (2)
 CC SEQUENCE FROM N.A. (ISOFORM 2).
 CC TISSUE=Medulla oblongata;
 CC MEDLINE=2238257; PubMed=12477932;
 CC Klausner R.D., Collins F.S., Wagner L., Spemmen C.M., Schuler G.D.,
 CC Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 CC Diatchenko L., Matulis A., Farmer A.A., Rubin G.M., Hong L.,
 CC Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 CC Brownstein M.J., Udell T.B., Tohyuki S., Carninci P., Prange C.,
 CC Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 CC Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 CC Villalón D.K., Murty D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 CC Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 CC Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 CC Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 CC Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 CC Butcherfield Y.S.N., Krzywicki M.I., Skala U., Smilins D.E.,
 CC Scheraga H., Schein J.E., Jones S.J.M., Marra M.A.,
 CC "Generation and initial analysis of more than 15,000 full-length human
 CC and mouse cDNA sequences."
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC [3]
 CC SEQUENCE OF 261-1088 FROM N.A. (ISOFORM 1).
 CC TISSUE=Brain;
 CC MEDLINE=20039619; PubMed=10574462;
 CC Nagase T., Ishikawa K.-I., Kikuno R., Hirosewa M., Nomura N.,
 CC Ohara O.;
 CC "Prediction of the coding sequences of unidentified human genes. XV.
 CC The complete sequences of 100 new cDNA clones from brain which code
 CC for large proteins in vitro."
 CC DNA Res. 6:337-345(1999).
 CC -1- FUNCTION: Poor transcriptional factor which uses the canonical
 CC single or multiple CARG boxes DNA sequence. Acts as a cofactor of
 CC serum response factor (SRF) with the potential to modulate SRF
 CC target genes (By similarity).
 CC -1- SUBUNIT: Interacts with SRF (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Comment=Full isoforms so far detected are isoform 2 and isoform
 CC 3;
 CC Name=1;
 CC IsoId=Q9ULH7-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9ULH7-2; Sequence=VSP_007653, VSP_007654, VSP_007655;
 CC Note=No experimental confirmation available;
 CC Name=3;
 CC IsoId=Q9ULH7-3; Sequence=VSP_007656, VSP_007657;
 CC Note=No experimental confirmation available;
 CC -1- DOMAIN: The N-terminal region is required for nuclear localization
 CC and the C-terminal region mediates transcriptional activity (By
 CC similarity).
 CC -1- SIMILARITY: Contains 3 RPEL repeats.
 CC -1- SIMILARITY: Contains 1 SAP domain.
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 CC -----
 CC EMBL: AK093577; BAC04200.1; -;
 CC EMBL: BC047761; AA047761.1; -;
 CC EMBL: AB033069; BA06557.2; -;
 CC InterPro: IPR004018; RPEL_repeat.
 CC InterPro: IPR003034; SAP.
 CC Pfam: PF02755; RPEL; 3.
 CC Pfam: PF02037; SAP; 1.
 CC SMART: SM00707; RPEL; 3.
 CC SMART: SM00513; SAP; 1.
 CC PROSITE: PS00800; SAP; 1.
 CC Transcription regulation; Nuclear protein; Coiled coil; Repeat;
 CC Alternative splicing.
 CC REPEAT 40 65
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 CC DOMAIN 671 787
 CC VARSPLIC 1 41
 CC --> M (in isoform 2).
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 CC DLKVSLEKTELKRGHPVSGTKEDLIERLPYQEVNSSGLA
 CC MVRVACIPROFLSKIGSEFLQVRNAPSOLFICILLEHQ
 CC NSTRCEKSVSSIIPIGINS (in isoform 2).
 CC /FTId=VSP_007654.
 CC Missing (in isoform 2).
 CC /FTId=VSP_007655.
 CC PLNDKNSNGSNALNNATPNTPTPRONTSTPRKRPGLPSSLD
 CC DLKVSLEKTELKRGHPVSGTKEDLIERLPYQEVNSSGLA
 CC AGGIVAVSSAIVTSNPEVTALPTTIN -> YGGAAHI
 CC LNRGSPVPRNRYKLEKVECHLFVSNDFPFIYAAHYI
 CC SEVHNVVACIPROFLSKIGSEFLQVRNAPSOLFICIL
 CC LEHONSTRCEKSVSSIIPIGINS (in isoform 3).
 CC /FTId=VSP_007656.
 CC Missing (in isoform 3).
 CC /FTId=VSP_007657.
 CC FT . CONFLICT 266 266 K -> R (in RRF. 1).
 CC SQ SEQUENCE 1088 AA; 118126 MW; 0CA4A52A115C0C83 CRC64;
 CC Query Match 77.3%; Score 34; DB 1; Length 1088;
 CC Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 1 KPSSPP 6
 CC Db 844 KPSSPP 849

Search completed: June 18, 2004, 12:58:58
 Job time : 16 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2004, 12:55:54 ; Search time 39 Seconds
(without alignments)
64.722 Million cell updates/sec

Title: US-10-655-201-2

Perfect score: 44

Sequence: 1 KPSPPEB 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 500 summaries

Database :

SPTREMBL_25:*
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*
15: sp_rv1rus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	93.2	566	10 Q8H611	Q8H611 zea mays (m
2	39	88.6	390	10 Q8R289	Q8R289 oryza sativ
3	39	88.6	802	10 Q8L775	Q8L775 arabidopsis
4	39	88.6	990	10 Q9LN08	Q9LN08 arabidopsis
5	38	86.4	87	15 Q38534	Q38534 human immun
6	38	86.4	215	11 Q9J0J3	Q9J0J3 mus musculu
7	38	86.4	216	4 Q8N5C9	Q8N5C9 homo sapien
8	38	86.4	460	11 Q8R4Z2	Q8R4Z2 mus musculu
9	38	86.4	460	11 Q8K4H6	Q8K4H6 mus musculu
10	38	86.4	461	4 Q96N03	Q96N03 mus musculu
11	38	86.4	607	10 Q9J0J7	Q9J0J7 homo sapien
12	38	86.4	607	10 Q9J0J7	Q9J0J7 arabidopsis
13	38	86.4	1351	3 Q872K5	Q872K5 neotospora
14	37	84.1	52	15 Q9J3Q8	Q9J3Q8 human immun
15	37	84.1	52	15 Q9J3S0	Q9J3S0 human immun
16	37	84.1	67	15 Q9IF19	Q9IF19 human immun

17	37	84.1	68	15 Q9DYK6	Q9DYK6 human immun
18	37	84.1	73	15 Q9IF25	Q9IF25 human immun
19	37	84.1	68	15 Q38224	Q38224 human immun
20	37	84.1	75	15 Q38232	Q38232 human immun
21	37	84.1	76	15 Q90QC3	Q90QC3 human immun
22	37	84.1	91	15 Q90QH2	Q90QH2 human immun
23	37	84.1	94	15 Q9DYQ4	Q9DYQ4 human immun
24	37	84.1	94	15 Q9DYQ1	Q9DYQ1 human immun
25	37	84.1	94	15 Q9DYQ7	Q9DYQ7 human immun
26	37	84.1	95	15 Q38202	Q38202 human immun
27	37	84.1	95	15 Q38182	Q38182 human immun
28	37	84.1	96	15 Q38195	Q38195 human immun
29	37	84.1	96	15 Q38214	Q38214 human immun
30	37	84.1	96	15 Q38215	Q38215 human immun
31	37	84.1	96	15 Q38208	Q38208 human immun
32	37	84.1	96	15 Q38218	Q38218 human immun
33	37	84.1	96	15 Q38210	Q38210 human immun
34	37	84.1	96	15 Q38193	Q38193 human immun
35	37	84.1	96	15 Q38183	Q38183 human immun
36	37	84.1	96	15 Q38204	Q38204 human immun
37	37	84.1	96	15 Q38221	Q38221 human immun
38	37	84.1	96	15 Q38205	Q38205 human immun
39	37	84.1	96	15 Q38206	Q38206 human immun
40	37	84.1	96	15 Q38198	Q38198 human immun
41	37	84.1	96	15 Q38207	Q38207 human immun
42	37	84.1	96	15 Q38197	Q38197 human immun
43	37	84.1	96	15 Q38184	Q38184 human immun
44	37	84.1	96	15 Q38194	Q38194 human immun
45	37	84.1	96	15 Q38200	Q38200 human immun
46	37	84.1	96	15 Q38211	Q38211 human immun
47	37	84.1	96	15 Q38181	Q38181 human immun
48	37	84.1	96	15 Q38216	Q38216 human immun
49	37	84.1	96	15 Q38213	Q38213 human immun
50	37	84.1	96	15 Q38222	Q38222 human immun
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53	37	84.1	96	15 Q38220	Q38220 human immun
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55	37	84.1	96	15 Q38192	Q38192 human immun
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58	37	84.1	96	15 Q38209	Q38209 human immun
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60	37	84.1	98	15 Q38227	Q38227 human immun
61	37	84.1	98	15 Q38234	Q38234 human immun
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66	37	84.1	111	15 Q38235	Q38235 human immun
67	37	84.1	113	15 Q75695	Q75695 human immun
68	37	84.1	113	15 Q38244	Q38244 human immun
69	37	84.1	113	15 Q38238	Q38238 human immun
70	37	84.1	113	15 Q38242	Q38242 human immun
71	37	84.1	113	15 Q38236	Q38236 human immun
72	37	84.1	120	17 Q87YP8	Q87YP8 mechanopryu
73	37	84.1	493	15 Q994M7	Q994M7 human immun
74	37	84.1	495	15 Q90157	Q90157 human immun
75	37	84.1	495	15 Q72J10	Q72J10 human immun
76	37	84.1	498	15 Q72J13	Q72J13 human immun
77	37	84.1	500	15 Q92897	Q92897 human immun
78	37	84.1	500	15 Q72626	Q72626 human immun
79	37	84.1	500	15 Q9J0H2	Q9J0H2 human immun
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84	37	84.1	500	15 Q8AUI5	Q8AUI5 human immun
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86	37	84.1	502	15 Q8A0W4	Q8A0W4 human immun
87	37	84.1	515	15 Q92900	Q92900 human immun
88	37	84.1	517	15 Q71261	Q71261 human immun
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91	37	84.1	562	5	Q8T0S2	Q8T0S2 dirosophila	164	35	79.5	1904	11	Q64699	Q64699 mus musc
92	37	84.1	833	5	Q8X0M6	Q8X0M6 neurospora	165	35	79.5	2137	4	Q15021	Q15021 homo sapien
93	37	84.1	846	5	Q8MRP6	Q8MRP6 dirosophila	166	34	77.3	17	4	Q9UEJ5	Q9UEJ5 homo sapien
94	37	84.1	1099	5	Q9VMS5	Q9VMS5 dirosophila	167	34	77.3	52	15	Q71399	Q71399 human immun
95	37	84.1	1109	5	Q9VAX4	Q9VAX4 dirosophila	168	34	77.3	56	15	Q7SEPR4	Q7SEPR4 human immun
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98	36	81.8	244	13	Q8UJH7	Q8UJH7 gallus gall	171	34	77.3	66	15	Q38530	Q38530 human immun
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102	36	81.8	275	13	Q7SXX7	Q7SXX7 brachydanio	175	34	77.3	67	15	Q38431	Q38431 human immun
103	36	81.8	362	4	Q13236	Q13236 homo sapien	176	34	77.3	67	15	Q9DYK3	Q9DYK3 human immun
104	36	81.8	442	10	Q7XN43	Q7XN43 oryza sativ	177	34	77.3	67	15	Q38295	Q38295 human immun
105	36	81.8	502	15	Q7ZJH8	Q7ZJH8 human immun	178	34	77.3	67	15	Q38429	Q38429 human immun
106	36	81.8	519	15	Q7ZJH8	Q7ZJH8 human immun	179	34	77.3	67	15	Q8AEW0	Q8AEW0 human immun
107	36	81.8	574	4	Q9NVB3	Q9NVB3 homo sapien	180	34	77.3	68	15	Q9DYK0	Q9DYK0 human immun
108	36	81.8	622	13	Q7ZMW5	Q7ZMW5 xenopus lae	181	34	77.3	68	15	Q38430	Q38430 human immun
109	36	81.8	655	11	Q9D2Z9	Q9D2Z9 mus musc	182	34	77.3	68	15	Q9DYK4	Q9DYK4 human immun
110	36	81.8	671	10	Q9FNA9	Q9FNA9 arabidopsis	183	34	77.3	68	15	Q9DYK1	Q9DYK1 human immun
111	36	81.8	698	16	Q83B86	Q83B86 coxiella bu	184	34	77.3	68	15	Q9DYK7	Q9DYK7 human immun
112	36	81.8	724	11	Q8BZM6	Q8BZM6 mus musc	185	34	77.3	69	15	Q9DYK2	Q9DYK2 human immun
113	36	81.8	816	16	Q8KT29	Q8KT29 ralestona, s	186	34	77.3	71	15	Q91F21	Q91F21 human immun
114	36	81.8	851	11	Q9CS19	Q9CS19 mus musc	187	34	77.3	73	15	Q38186	Q38186 human immun
115	36	81.8	877	11	Q8K332	Q8K332 mus musc	188	34	77.3	73	15	Q38428	Q38428 human immun
116	36	81.8	1154	4	Q9P2P0	Q9P2P0 homo sapien	189	34	77.3	73	15	Q38188	Q38188 human immun
117	36	81.8	1185	4	Q9NTD2	Q9NTD2 homo sapien	190	34	77.3	73	15	Q38187	Q38187 human immun
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120	36	81.8	1431	4	Q8WAD9	Q8WAD9 homo sapien	193	34	77.3	74	15	Q9DYK2	Q9DYK2 human immun
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124	35	79.5	120	4	Q95608	Q95608 homo sapien	197	34	77.3	75	15	Q38491	Q38491 human immun
125	35	79.5	189	11	Q8CG36	Q8CG36 mus sp. fib	198	34	77.3	77	15	Q90Q16	Q90Q16 human immun
126	35	79.5	215	5	Q26880	Q26880 trypanosoma	199	34	77.3	77	15	Q38442	Q38442 human immun
127	35	79.5	216	5	Q45932	Q45932 caenorhabdi	200	34	77.3	77	15	Q38436	Q38436 human immun
128	35	79.5	219	12	Q8QHR9	Q8QHR9 influenza a	201	34	77.3	77	15	Q90QG8	Q90QG8 human immun
129	35	79.5	249	12	Q92435	Q92435 bombyx mori	202	34	77.3	78	15	Q91F15	Q91F15 human immun
130	35	79.5	267	11	Q9D255	Q9D255 mus musc	203	34	77.3	78	15	Q38450	Q38450 human immun
131	35	79.5	320	6	Q9SKY4	Q9SKY4 bos taurus	204	34	77.3	78	15	Q38433	Q38433 human immun
132	35	79.5	347	6	Q9SKV5	Q9SKV5 bos taurus	205	34	77.3	78	15	Q38440	Q38440 human immun
133	35	79.5	354	4	Q9U0S6	Q9U0S6 homo sapien	206	34	77.3	78	15	Q38468	Q38468 human immun
134	35	79.5	374	10	Q39307	Q39307 brassica na	207	34	77.3	78	15	Q38449	Q38449 human immun
135	35	79.5	376	10	Q39306	Q39306 mus musc	208	34	77.3	78	15	Q90QC7	Q90QC7 human immun
136	35	79.5	378	11	Q99KM7	Q99KM7 mus musc	209	34	77.3	78	15	Q38469	Q38469 human immun
137	35	79.5	379	4	Q95617	Q95617 homo sapien	210	34	77.3	78	15	Q38434	Q38434 human immun
138	35	79.5	382	13	Q7ZVT0	Q7ZVT0 brachydanio	211	34	77.3	78	15	Q38124	Q38124 human immun
139	35	79.5	407	17	Q29718	Q29718 archaeoglob	212	34	77.3	78	15	Q90QG4	Q90QG4 human immun
140	35	79.5	440	13	Q90816	Q90816 gallus gall	213	34	77.3	78	15	Q90QH6	Q90QH6 human immun
141	35	79.5	446	4	Q8N3Y0	Q8N3Y0 homo sapien	214	34	77.3	78	15	Q38437	Q38437 human immun
142	35	79.5	471	11	Q9D3R9	Q9D3R9 mus musc	215	34	77.3	78	15	Q90QC9	Q90QC9 human immun
143	35	79.5	486	16	Q8BDN2	Q8BDN2 synchococc	216	34	77.3	79	15	Q38467	Q38467 human immun
144	35	79.5	504	10	Q9LH00	Q9LH00 arabidopsis	217	34	77.3	79	15	Q38441	Q38441 human immun
145	35	79.5	507	5	Q968L9	Q968L9 trypanosoma	218	34	77.3	79	15	Q38435	Q38435 human immun
146	35	79.5	516	10	Q9SLH0	Q9SLH0 arabidopsis	219	34	77.3	79	15	Q90QCS	Q90QCS human immun
147	35	79.5	539	10	Q941P5	Q941P5 arabidopsis	220	34	77.3	79	15	Q90QES	Q90QES human immun
148	35	79.5	539	10	Q8L787	Q8L787 arabidopsis	221	34	77.3	79	15	Q38448	Q38448 human immun
149	35	79.5	558	3	Q13330	Q13330 emericella	222	34	77.3	79	15	Q90QD8	Q90QD8 human immun
150	35	79.5	609	17	Q8TXA4	Q8TXA4 methanopyru	223	34	77.3	79	15	Q38471	Q38471 human immun
151	35	79.5	776	11	Q8K1N1	Q8K1N1 mus musc	224	34	77.3	80	15	Q38439	Q38439 human immun
152	35	79.5	784	11	Q8C605	Q8C605 mus musc	225	34	77.3	80	15	Q90QH4	Q90QH4 human immun
153	35	79.5	784	11	Q8C516	Q8C516 mus musc	226	34	77.3	80	15	Q90QD5	Q90QD5 human immun
154	35	79.5	803	11	Q9DC20	Q9DC20 mus musc	227	34	77.3	81	15	Q90Q10	Q90Q10 human immun
155	35	79.5	810	11	Q8R3F3	Q8R3F3 mus musc	228	34	77.3	81	15	Q38457	Q38457 human immun
156	35	79.5	922	11	Q8BZX2	Q8BZX2 mus musc	229	34	77.3	82	15	Q90QJ2	Q90QJ2 human immun
157	35	79.5	1157	1	Q9HH42	Q9HH42 methanobact	230	34	77.3	82	15	Q38456	Q38456 human immun
158	35	79.5	1179	16	Q9RVV9	Q9RVV9 deinococcus	231	34	77.3	84	15	Q38477	Q38477 human immun
159	35	79.5	1186	9	Q80211	Q80211 methanobact	232	34	77.3	86	15	Q38289	Q38289 human immun
160	35	79.5	1399	4	Q75870	Q75870 homo sapien	233	34	77.3	86	15	Q38459	Q38459 human immun
161	35	79.5	1863	11	Q64605	Q64605 rattus norv	234	34	77.3	86	15	Q38517	Q38517 human immun
162	35	79.5	1894	11	Q64487	Q64487 mus musc	235	34	77.3	86	15	Q38037	Q38037 human immun

236	34	77.3	86	15	038306	038306	human	immun	309	34	77.3	86	15	038458	038458	human	immun
237	34	77.3	86	15	038452	038452	human	immun	310	34	77.3	86	15	038278	038278	human	immun
238	34	77.3	86	15	038460	038460	human	immun	311	34	77.3	86	15	038325	038325	human	immun
239	34	77.3	86	15	038331	038331	human	immun	312	34	77.3	86	15	038248	038248	human	immun
240	34	77.3	86	15	038297	038297	human	immun	313	34	77.3	86	15	038308	038308	human	immun
241	34	77.3	86	15	038317	038317	human	immun	314	34	77.3	86	15	038290	038290	human	immun
242	34	77.3	86	15	038038	038038	human	immun	315	34	77.3	86	15	038536	038536	human	immun
243	34	77.3	86	15	038446	038446	human	immun	316	34	77.3	86	15	038304	038304	human	immun
244	34	77.3	86	15	038489	038489	human	immun	317	34	77.3	86	15	038268	038268	human	immun
245	34	77.3	86	15	038263	038263	human	immun	318	34	77.3	86	15	038301	038301	human	immun
246	34	77.3	86	15	038272	038272	human	immun	319	34	77.3	86	15	038275	038275	human	immun
247	34	77.3	86	15	038535	038535	human	immun	320	34	77.3	86	15	038462	038462	human	immun
248	34	77.3	86	15	038246	038246	human	immun	321	34	77.3	86	15	038497	038497	human	immun
249	34	77.3	86	15	038039	038039	human	immun	322	34	77.3	86	15	038334	038334	human	immun
250	34	77.3	86	15	038293	038293	human	immun	323	34	77.3	86	15	038287	038287	human	immun
251	34	77.3	86	15	038280	038280	human	immun	324	34	77.3	86	15	038264	038264	human	immun
252	34	77.3	86	15	038318	038318	human	immun	325	34	77.3	86	15	038245	038245	human	immun
253	34	77.3	86	15	038455	038455	human	immun	326	34	77.3	86	15	038283	038283	human	immun
254	34	77.3	86	15	038262	038262	human	immun	327	34	77.3	86	15	038533	038533	human	immun
255	34	77.3	86	15	038256	038256	human	immun	328	34	77.3	86	15	038252	038252	human	immun
256	34	77.3	86	15	038273	038273	human	immun	329	34	77.3	86	15	038323	038323	human	immun
257	34	77.3	86	15	038322	038322	human	immun	330	34	77.3	86	15	038277	038277	human	immun
258	34	77.3	86	15	038253	038253	human	immun	331	34	77.3	86	15	038324	038324	human	immun
259	34	77.3	86	15	038288	038288	human	immun	332	34	77.3	86	15	038305	038305	human	immun
260	34	77.3	86	15	038531	038531	human	immun	333	34	77.3	86	15	038254	038254	human	immun
261	34	77.3	86	15	038036	038036	human	immun	334	34	77.3	86	15	038247	038247	human	immun
262	34	77.3	86	15	038332	038332	human	immun	335	34	77.3	86	15	038309	038309	human	immun
263	34	77.3	86	15	038270	038270	human	immun	336	34	77.3	86	15	038282	038282	human	immun
264	34	77.3	86	15	038035	038035	human	immun	337	34	77.3	86	15	038515	038515	human	immun
265	34	77.3	86	15	038281	038281	human	immun	338	34	77.3	86	15	038444	038444	human	immun
266	34	77.3	86	15	038330	038330	human	immun	339	34	77.3	86	15	038426	038426	human	immun
267	34	77.3	86	15	038327	038327	human	immun	340	34	77.3	86	15	038481	038481	human	immun
268	34	77.3	86	15	038250	038250	human	immun	341	34	77.3	86	15	038500	038500	human	immun
269	34	77.3	86	15	038328	038328	human	immun	342	34	77.3	86	15	038496	038496	human	immun
270	34	77.3	86	15	038326	038326	human	immun	343	34	77.3	86	15	038427	038427	human	immun
271	34	77.3	86	15	038298	038298	human	immun	344	34	77.3	86	15	038461	038461	human	immun
272	34	77.3	86	15	038451	038451	human	immun	345	34	77.3	86	15	038425	038425	human	immun
273	34	77.3	86	15	038529	038529	human	immun	346	34	77.3	86	15	038465	038465	human	immun
274	34	77.3	86	15	038315	038315	human	immun	347	34	77.3	86	15	038513	038513	human	immun
275	34	77.3	86	15	038463	038463	human	immun	348	34	77.3	86	15	038484	038484	human	immun
276	34	77.3	86	15	038251	038251	human	immun	349	34	77.3	86	15	038512	038512	human	immun
277	34	77.3	86	15	038320	038320	human	immun	350	34	77.3	86	15	038447	038447	human	immun
278	34	77.3	86	15	038279	038279	human	immun	351	34	77.3	86	15	038502	038502	human	immun
279	34	77.3	86	15	038302	038302	human	immun	352	34	77.3	86	15	038464	038464	human	immun
280	34	77.3	86	15	038333	038333	human	immun	353	34	77.3	86	15	038528	038528	human	immun
281	34	77.3	86	15	038259	038259	human	immun	354	34	77.3	86	15	038474	038474	human	immun
282	34	77.3	86	15	038313	038313	human	immun	355	34	77.3	86	15	038486	038486	human	immun
283	34	77.3	86	15	038490	038490	human	immun	356	34	77.3	86	15	038501	038501	human	immun
284	34	77.3	86	15	038291	038291	human	immun	357	34	77.3	86	15	038480	038480	human	immun
285	34	77.3	86	15	038261	038261	human	immun	358	34	77.3	86	15	038472	038472	human	immun
286	34	77.3	86	15	038307	038307	human	immun	359	34	77.3	86	15	038479	038479	human	immun
287	34	77.3	86	15	038255	038255	human	immun	360	34	77.3	86	15	038510	038510	human	immun
288	34	77.3	86	15	038303	038303	human	immun	361	34	77.3	86	15	038470	038470	human	immun
289	34	77.3	86	15	038319	038319	human	immun	362	34	77.3	86	15	038493	038493	human	immun
290	34	77.3	86	15	038260	038260	human	immun	363	34	77.3	86	15	038482	038482	human	immun
291	34	77.3	86	15	038505	038505	human	immun	364	34	77.3	86	15	038538	038538	human	immun
292	34	77.3	86	15	038454	038454	human	immun	365	34	77.3	86	15	038503	038503	human	immun
293	34	77.3	86	15	038271	038271	human	immun	366	34	77.3	86	15	038518	038518	human	immun
294	34	77.3	86	15	038296	038296	human	immun	367	34	77.3	86	15	038478	038478	human	immun
295	34	77.3	86	15	038249	038249	human	immun	368	34	77.3	86	15	038494	038494	human	immun
296	34	77.3	86	15	038258	038258	human	immun	369	34	77.3	86	15	038514	038514	human	immun
297	34	77.3	86	15	038265	038265	human	immun	370	34	77.3	86	15	038509	038509	human	immun
298	34	77.3	86	15	038519	038519	human	immun	371	34	77.3	86	15	038508	038508	human	immun
299	34	77.3	86	15	038314	038314	human	immun	372	34	77.3	86	15	038485	038485	human	immun
300	34	77.3	86	15	038266	038266	human	immun	373	34	77.3	86	15	038537	038537	human	immun
301	34	77.3	86	15	038312	038312	human	immun	374	34	77.3	86	15	038504	038504	human	immun
302	34	77.3	86	15	038453	038453	human	immun	375	34	77.3	86	15	038483	038483	human	immun
303	34	77.3	86	15	038311	038311	human	immun	376	34	77.3	86	15	038507	038507	human	immun
304	34	77.3	86	15	038532	038532	human	immun	377	34	77.3	86	15	038466	038466	human	immun
305	34	77.3	86	15	038321	038321	human	immun	378	34	77.3	86	15	038475	038475	human	immun
306	34	77.3	86	15	038276	038276	human	immun	379	34	77.3	86	15	038473	038473	human	immun
307	34	77.3	86	15	038274	038274	human	immun	380	34	77.3	86	15	038445	038445	human	immun
308	34	77.3	86	15	038267	038267	human	immun	381	34	77.3	86	15	038511	038511	human	immun

382	34	77.3	88	15	038476	038476	human	immun
383	34	77.3	88	15	038495	038495	human	immun
384	34	77.3	88	15	038498	038498	human	immun
385	34	77.3	88	15	038499	038499	human	immun
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388	34	77.3	88	15	038510	038510	human	immun
389	34	77.3	89	15	038517	038517	human	immun
390	34	77.3	91	15	038518	038518	human	immun
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392	34	77.3	92	15	038520	038520	human	immun
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395	34	77.3	93	15	038523	038523	human	immun
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413	34	77.3	94	15	038541	038541	human	immun
414	34	77.3	94	15	038542	038542	human	immun
415	34	77.3	94	15	038543	038543	human	immun
416	34	77.3	94	15	038544	038544	human	immun
417	34	77.3	94	15	038545	038545	human	immun
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451	34	77.3	94	15	038579	038579	human	immun
452	34	77.3	94	15	038580	038580	human	immun
453	34	77.3	94	15	038581	038581	human	immun
454	34	77.3	94	15	038582	038582	human	immun

RESULT 1
 ID Q8H611 PRELIMINARY; PRT; 566 AA.
 AC Q8H611; 01-MAR-2003 (TREMblrel. 23, Created)
 DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
 DE Putative MURAZC.
 GN ZMR5072.18.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. BSSS53;
 RX MEDLINE=2253764; PubMed=12368247;
 RA Song R., Llaica V., Messing J.;
 RT "Kobasi Organization of Orthologous Sequences in Grass Genomes";
 RL Genome Res. 12:1549-1555(2002).
 DR EMBL; AF528565; AAN40034.1; -.

ALIGNMENTS

455	34	77.3	94	15	Q9DYS0	Q9DYS0	human	immun
456	34	77.3	94	15	Q9DZ07	Q9DZ07	human	immun
457	34	77.3	94	15	Q9DZ01	Q9DZ01	human	immun
458	34	77.3	94	15	Q9DZ75	Q9DZ75	human	immun
459	34	77.3	95	15	Q9DZ75	Q9DZ75	human	immun
460	34	77.3	95	15	Q9DZ20	Q9DZ20	human	immun
461	34	77.3	95	15	Q9DZ17	Q9DZ17	human	immun
462	34	77.3	96	15	Q9DZ13	Q9DZ13	human	immun
463	34	77.3	96	15	Q9DZ16	Q9DZ16	human	immun
464	34	77.3	96	15	Q9DZ19	Q9DZ19	human	immun
465	34	77.3	96	15	Q9DZ17	Q9DZ17	human	immun
466	34	77.3	96	15	Q9DZ14	Q9DZ14	human	immun
467	34	77.3	96	15	Q9DZ16	Q9DZ16	human	immun
468	34	77.3	96	15	Q9DZ10	Q9DZ10	human	immun
469	34	77.3	96	15	Q9DZ69	Q9DZ69	human	immun
470	34	77.3	96	15	Q9DZ19	Q9DZ19	human	immun
471	34	77.3	96	15	Q9DZ14	Q9DZ14	human	immun
472	34	77.3	96	15	Q9DZ92	Q9DZ92	human	immun
473	34	77.3	96	15	Q9DZ16	Q9DZ16	human	immun
474	34	77.3	96	15	Q9DZ11	Q9DZ11	human	immun
475	34	77.3	96	15	Q9DZ10	Q9DZ10	human	immun
476	34	77.3	96	15	Q9DZ16	Q9DZ16	human	immun
477	34	77.3	96	15	Q9DZ10	Q9DZ10	human	immun
478	34	77.3	96	15	Q9DZ10	Q9DZ10	human	immun
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493	34	77.3	97	15	Q9DZ15	Q9DZ15	human	immun
494	34	77.3	97	15	Q9DZ15	Q9DZ15	human	immun
495	34	77.3	97	15	Q9DZ15	Q9DZ15	human	immun
496	34	77.3	97	15	Q9DZ15	Q9DZ15	human	immun
497	34	77.3	98	15	Q9DZ15	Q9DZ15	human	immun
498	34	77.3	99	15	Q9DZ15	Q9DZ15	human	immun
499	34	77.3	99	15	Q9DZ15	Q9DZ15	human	immun
500	34	77.3	99	15	Q9DZ15	Q9DZ15	human	immun

DR InterPro: IPR001207; Trnspase_mutatr.
 DR InterPro: IPR006564; Znf_PWZ.
 DR InterPro: IPR007527; Znf_SWIM.
 DR Pfam: PF04434; SWIM, 1.
 DR SMART: SM00575; Znf_PWZ, 1.
 DR PROSITE: PS01007; TRANSPOSASE_MUTATOR, 1.
 SQ SEQUENCE 566 AA; 65236 MW; AF06A33C0A3E8C36 CRC64;

Query Match 93.2%; Score 41; DB 10; Length 566;
 Best Local Similarity 87.5%; Pred. No. 38;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPSSPPE 8
 Db 542 RPSSPPE 549

RESULT 2

Q8R289 PRELIMINARY; PRT; 390 AA.
 AC Q8R289;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE OSJNB0063G05.9 protein.
 GN OSJNB0063G05.9.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
 RT clone:OSJNB0063G05.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF003760; BAB90500.1; -.
 DR Gramene; Q8R289; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0016462; F:pyrophosphatase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro: IPR008162; Pyrophosphatase.
 DR PROSITE: PS00387; PASE; 1.
 SQ SEQUENCE 390 AA; 43198 MW; 23CE65ED8A3745A0 CRC64;

Query Match 88.6%; Score 39; DB 10; Length 390;
 Best Local Similarity 100.0%; Pred. No. 58;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 PSSPPE 8
 Db 231 PSSPPE 237

RESULT 3

Q8L775 PRELIMINARY; PRT; 802 AA.
 AC Q8L775;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE At1g07990/TED22.5.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shim P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
 RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.C., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Becker J.R.;
 RT "Arabidopsis cDNA clones."
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Shim P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Heuan V.W.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
 RA Palm C.C., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,
 RA Shinozaki K., Davis R.W., Theologis A., Becker J.R.;
 RT "Arabidopsis ORF clones."
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY127028; AAM83251.1; -.
 DR EMBL: BT004535; AAO42781.1; -.
 DR InterPro: IPR007587; SAPS.
 DR Pfam: PF04499; SAPS; 1.
 SQ SEQUENCE 802 AA; 89588 MW; 705F6276049B4F32 CRC64;

Query Match 88.6%; Score 39; DB 10; Length 802;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPSSPPE 7
 Db 202 KPSSPPE 208

RESULT 4

Q9JN08 PRELIMINARY; PRT; 990 AA.
 AC Q9JN08;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE TED22.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Shim P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
 RA Kim C., Altafi H., Bel O., Chin C., Chou J., Choi B., Conn L.,
 RA Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharly N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thavert A.,
 RA Toriumi M., Vayberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Becker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC TED22 from chromosome
 RT 1."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RA Becker J.R.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]

RP SEQUENCE FROM N.A.
 RA Cheuk R., Shim P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bel B., Chin C., Chou J., Choi E.,
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharly N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,

RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC026875; AAF79824.1; -.
 DR PIR: A86215; A86215.
 DR InterPro: IPR007587; SAPS.
 DR Pfam: PF04499; SAPS; 1.
 SQ SEQUENCE 990 AA; 110996 MW; E86B7D5C04D298E CRC64;

Query Match 86.4%; Score 39; DB 10; Length 990;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 7
 Db 381 KPSSPPE 387

RESULT 5

ID 038534 PRELIMINARY; PRT; 87 AA.
 AC 038534;
 DT 01-JUN-1998 (TEMBLrel. 05, Created)
 DT 01-JUN-1998 (TEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404676; Pubmed=9261388;
 RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
 RA Vasudevarchari M.B., Salzman N.P.;
 RT "drug resistance during indinavir therapy is caused by mutations in
 RT the protease gene and in its Gag substrate cleavage sites.";
 RL J. Virol. 71:6662-6670(1997).
 DR EMBL: AF024433; AAB83307.1; -.
 DR HSP: P05888; IAAF.
 DR GO: GO:0019012; Cytolysis; IEA.
 DR GO: GO:0003676; F: nucleic acid binding; IEA.
 DR InterPro: IPR001878; ZnF_CCHC.
 DR Pfam: PF00098; Zf-CCHC; 1.
 DR PRINTS: SM00343; ZnF_C2HC; 1.
 DR SMART: SM00343; ZnF_C2HC; 1.
 DR PROSITE: PS50158; ZF_CCHC; 1.
 KM Core protein; Polyprotein.
 FT NON_TER 1
 FT NON_TER 87
 SQ SEQUENCE 87 AA; 10037 MW; C0525F43D8210973 CRC64;

Query Match 86.4%; Score 38; DB 15; Length 87;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
 Db 53 KPAPPEE 60

RESULT 6

ID 099303 PRELIMINARY; PRT; 215 AA.
 AC 099303;
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Similar to hypothetical protein FLJ20837.
 GN SLC30A6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC005753; AAH05753.1; -.
 DR MGI: MGI:2386741; SLC30A6.
 DR GO: GO:0005385; F: zinc ion transporter activity; IDA.
 DR GO: GO:0006829; P: zinc ion transport; IDA.
 DR GO: GO:0006829; P: zinc ion transport; IDA.
 DR InterPro: IPR002524; Cation_efflux; 1.
 DR Pfam: PF01545; Cation_efflux; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 215 AA; 23529 MW; 9B58AFC6C2B3872 CRC64;

Query Match 86.4%; Score 38; DB 11; Length 215;
 Best Local Similarity 87.5%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
 Db 134 KPSSPPE 141

RESULT 7

ID 08N5C9 PRELIMINARY; PRT; 216 AA.
 AC 08N5C9;
 DT 01-OCT-2002 (TEMBLrel. 22, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE Similar to hypothetical protein MGC11963.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC032525; AAH32525.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 216 AA; 23562 MW; DD7E7F862B788FB3 CRC64;

Query Match 86.4%; Score 38; DB 4; Length 216;
 Best Local Similarity 87.5%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
 Db 134 KPSSPPE 141

RESULT 8

ID 08R422 PRELIMINARY; PRT; 460 AA.
 AC 08R422;
 DT 01-JUN-2002 (TEMBLrel. 21, Created)
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Zinc transporter-like 3 protein.
 GN SLC30A6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Zhu W., Mager S.;
 RT "Cloning of new mammalian zinc transporter-like genes."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF233346; AAL8317.1; -.
 DR MGD; MGI:2386741; SLC30A6.
 DR GO; GO:0005385; P:zinc ion transporter activity; IDA.
 DR GO; GO:0006895; P:golgi to endosome transport; IDA.
 DR GO; GO:0006829; P:zinc ion transport; IDA.
 DR InterPro; IPR002524; Cation_efflux.
 DR Pfam; PF01545; Cation_efflux; 1.
 DR TIGRPFAM; TIGR01297; CDF; 1.
 SQ SEQUENCE 460 AA; 51015 MW; A05DD3116E0BC051 CRC64;

Query Match 86.4%; Score 38; DB 11; Length 460;
 Best Local Similarity 87.5%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSSPPEE 8
 DB 379 KPSSPPEE 386

RESULT 9
 ID Q8K4H6 PRELIMINARY; PRT; 460 AA.

AC Q8K4H6; 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Zinc transporter 6.
 GN SLC30A6 OR ZNT6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J;
 RX MEDLINE=22113027; PubMed=11997387;
 RA Huang L., Kirschke C.P., Gitchever J.;
 RT "Functional Characterization of a Novel Mammalian Zinc Transporter,
 ZNT6";
 RL J. Biol. Chem. 277:26389-26395(2002).
 DR EMBL; AF395840; AAM27917.1; -.
 DR MGD; MGI:2386741; SLC30A6.
 DR GO; GO:0005385; P:zinc ion transporter activity; IDA.
 DR GO; GO:0006895; P:golgi to endosome transport; IDA.
 DR GO; GO:0006829; P:zinc ion transport; IDA.
 DR InterPro; IPR002524; Cation_efflux.
 DR Pfam; PF01545; Cation_efflux; 1.
 DR TIGRPFAM; TIGR01297; CDF; 1.
 SQ SEQUENCE 460 AA; 50894 MW; B61A2F0E0AD6921B CRC64;

Query Match 86.4%; Score 38; DB 11; Length 460;
 Best Local Similarity 87.5%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSSPPEE 8
 DB 379 KPSSPPEE 386

RESULT 10
 ID Q8BJM5 PRELIMINARY; PRT; 460 AA.

AC Q8BJM5; 01-MAR-2003 (T-EMBLrel. 23, Created)
 DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE CDNA FLJ31101 FIS.
 GN SLC30A6.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Body;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 DR EMBL; AK082807; BAC3680.1; -.
 DR MGD; MGI:2386741; SLC30A6.
 DR GO; GO:0005385; P:zinc ion transporter activity; IDA.
 DR GO; GO:0006895; P:golgi to endosome transport; IDA.
 DR GO; GO:0006829; P:zinc ion transport; IDA.
 DR InterPro; IPR002524; Cation_efflux.
 DR Pfam; PF01545; Cation_efflux; 1.
 DR TIGRPFAM; TIGR01297; CDF; 1.
 SQ SEQUENCE 460 AA; 51026 MW; A3B910CB96D16015 CRC64;

Query Match 86.4%; Score 38; DB 11; Length 460;
 Best Local Similarity 87.5%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSSPPEE 8
 DB 379 KPSSPPEE 386

RESULT 11
 ID Q96NC3 PRELIMINARY; PRT; 461 AA.

AC Q96NC3; 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Hypothetical protein FLJ31101.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
 RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hiro Y., Saio K., Nishikawa T., Kimura K., Yanagita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagaesuma M.,
 RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
 RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
 RA Isegaki T.;
 RT "NEDO human cDNA sequencing project";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK055663; BAB70980.1; -.
 DR Genew; HGNC:19305; SLC30A6.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008324; P:cation transporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR002524; Cation_efflux.
 DR Pfam; PF01545; Cation_efflux; 1.
 DR TIGRPFAM; TIGR01297; CDF; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 461 AA; 51115 MW; 7926F6888EF1F1F9 CRC64;

Query Match 86.4%; Score 38; DB 4; Length 461;
 Best Local Similarity 87.5%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KPSSPPEE 8
 DB 379 KPSSPPEE 386

RESULT 12
 Q9LUT9

ID 09L079 PRELIMINARY; PRT; 607 AA.
 AC 09L079;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TEMBLrel. 25, Last annotation update)
 DE Db|AA21150.1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 RT clones."
 RL DNA Res. 7:31-63(2000).
 DR EMBL; AB023042; BAA97357.1; -.
 SQ SEQUENCE 607 AA; 67287 MW; C67FE8C2F21D9317 CRC64;

Query Match 86.4%; Score 38; DB 10; Length 607;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
 Db 240 KPSSPPEE 247

RESULT 13

ID 0872R5 PRELIMINARY; PRT; 1351 AA.
 AC 0872R5;
 DT 01-JUN-2003 (TEMBLrel. 24, Created)
 DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Related to RNA-directed RNA polymerase.
 GN B13B3.100.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project,
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX284762; CAD70515.1; -.
 DR GO; GO:0016329; F:apoptosis regulator activity; IEA.
 DR GO; GO:000368; F:RNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0006915; P:apoptosis; IEA.
 DR InterPro; IPR000712; Bcl2_BH.
 DR InterPro; IPR007855; RGRP.
 DR InterPro; IPR003124; WH2.
 DR Pfam; PF05183; RGRP.1.
 DR Pfam; PF02205; WH2.1.
 DR PROSITE; PS01259; BH3.1.
 KM RNA-directed RNA polymerase.
 SQ SEQUENCE 1351 AA; 151975 MW; 0C784B99CDC66AB6 CRC64;

Query Match 86.4%; Score 38; DB 3; Length 1351;
 Best Local Similarity 75.0%; Pred. No. 3.1e+02;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8

Db 1132 RPSTPPEE 1139

RESULT 14

ID 099308 PRELIMINARY; PRT; 52 AA.
 AC 099308;
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B497;
 RX MEDLINE=21136890; PubMed=11238855;
 RA Biebler G., Munoz M., Cluffi A., Meylan P., Telenti A.;
 RT "Individual Contributions of Mutant Protease and Reverse Transcriptase
 RT to Viral Infectivity, Replication, and Protein Maturation of
 RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1."
 RL J. Virol. 75:3291-3300(2001).
 DR EMBL; AF316838; AAK21082.1; -.
 FT NON_TER
 SQ SEQUENCE 52 AA; 5704 MW; 1312CE4A8CF0D75 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 52;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
 Db 6 EPSAPPEE 13

RESULT 15

ID 099350 PRELIMINARY; PRT; 52 AA.
 AC 099350;
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B495;
 RX MEDLINE=21136890; PubMed=11238855;
 RA Biebler G., Munoz M., Cluffi A., Meylan P., Telenti A.;
 RT "Individual Contributions of Mutant Protease and Reverse Transcriptase
 RT to Viral Infectivity, Replication, and Protein Maturation of
 RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1."
 RL J. Virol. 75:3291-3300(2001).
 DR EMBL; AF316831; AAK21070.1; -.
 FT NON_TER
 SQ SEQUENCE 52 AA; 5719 MW; 47C0789171E09693 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 52;
 Best Local Similarity 75.0%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
 Db 6 EPSAPPEE 13

RESULT 16

091F19
ID 091F19 PRELIMINARY; PRT; 67 AA.
AC 091F19;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1145;
RX MEDLINE=21443958; PubMed=11559796;
RA Peters S., Munoz M., Yerly S., Sanchez-Merino V., Lopez-Galindez C.,
RA Perrin L., Larder B., Cmarko D., Fakan S., Maylan P., Telenti A.;
RT "Resistance to Nucleoside Analog Reverse Transcriptase Inhibitors
Mediated by Human Immunodeficiency Virus Type 1 p6 Protein.";
RL J. Virol. 75:9644-9653(2001).
DR EMBL; AF282962; AAF87816.1; -.
FT NON_TER 1 1
SQ SEQUENCE 67 AA; 7470 MW; 810C3A06512E9A65 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 67;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
Db 22 EPSAPPEE 29

RESULT 17
ID 09DYK6 PRELIMINARY; PRT; 68 AA.
AC 09DYK6;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2016;
RA Telenti A., Martinez R., Peters S.;
RT "Natural mutants of HIV-1 subtype B frameshift gag p1 stemloop.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF293421; AAG15244.1; -.
FT NON_TER 1 1
FT VARIANT 9 9 N -> Y.
SQ SEQUENCE 68 AA; 7546 MW; 03E7B81A6F742393 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 68;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
Db 22 EPSAPPEE 29

RESULT 18
ID 09IF25 PRELIMINARY; PRT; 68 AA.
AC 09IF25;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).

GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1186;
RX MEDLINE=21443958; PubMed=11559796;
RA Peters S., Munoz M., Yerly S., Sanchez-Merino V., Lopez-Galindez C.,
RA Perrin L., Larder B., Cmarko D., Fakan S., Maylan P., Telenti A.;
RT "Resistance to Nucleoside Analog Reverse Transcriptase Inhibitors
Mediated by Human Immunodeficiency Virus Type 1 p6 Protein.";
RL J. Virol. 75:9644-9653(2001).
DR EMBL; AF282959; AAF87810.1; -.
FT NON_TER 1 1
SQ SEQUENCE 68 AA; 7585 MW; 8F1F542E831A3DD1 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 68;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
Db 22 EPSAPPEE 29

RESULT 19
ID 038224 PRELIMINARY; PRT; 73 AA.
AC 038224;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024121; AAB82997.1; -.
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR SMART; SM00343; Znf_CCHC; 1.
KW Core protein; PolyProtein.
FT NON_TER 1 1
FT NON_TER 73 73
SQ SEQUENCE 73 AA; 8224 MW; 2EA56BD672D4153 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 73;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
Db 39 EPSAPPEE 46

RESULT 20
ID 038232 PRELIMINARY; PRT; 75 AA.
AC 038232;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).

GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamiuchi H., Imamiuchi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
EMBL: AF024129; AAB83005.1; -.
DR GO: 0019012; C:violin; IEA.
DR GO: 0003676; F:nucleic acid binding; IEA.
DR InterPro: IPR001878; Znf_CCHC.
DR SMART: SM00343; Znf_CCHC; 1.
KM Core protein; Polyprotein.
FT NON_TER 1
FT SEQUENCE 75 AA; 8504 MW; 7F9E6A43622C92BF CRC64;
SQ

Query Match 84.1%; Score 37; DB 15; Length 75;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
Db 39 EPSAPPEE 46

RESULT 21

Q90QC3 PRELIMINARY; PRT; 76 AA.

ID Q90QC3
AC Q90QC3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=11248068; PubMed=11350662;
RA Kaufmann G.R., Suzuki K., Cunningham P., Mukai M., Kondo M.,
RA Imai M., Zaunders J., Cooper D.A.;
RT "Impact of HIV Type 1 Protease, Reverse Transcriptase, Cleavage Site,
and p6 Mutations on the Virological Response to Quadruple Therapy with
Ritonavir, Zidovudine, and Two Nucleoside Analogs.";
RT AIDS Res. Hum. Retroviruses 17:487-497(2001).
RL AIDS Res. Hum. Retroviruses 17:487-497(2001).
DR EMBL: AF323242; AAK66729.1; -.
FT NON_TER 1
FT SEQUENCE 76 AA; 8558 MW; 8BD09026451B1B90 CRC64;
SQ

Query Match 84.1%; Score 37; DB 15; Length 76;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
Db 30 EPSAPPEE 37

RESULT 22

Q90QH2 PRELIMINARY; PRT; 91 AA.

ID Q90QH2
AC Q90QH2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).

GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=11248068; PubMed=11350662;
RA Kaufmann G.R., Suzuki K., Cunningham P., Mukai M., Kondo M.,
RA Imai M., Zaunders J., Cooper D.A.;
RT "Impact of HIV Type 1 Protease, Reverse Transcriptase, Cleavage Site,
and p6 Mutations on the Virological Response to Quadruple Therapy with
Ritonavir, Zidovudine, and Two Nucleoside Analogs.";
RL AIDS Res. Hum. Retroviruses 17:487-497(2001).
EMBL: AF323216; AAK66680.1; -.
DR GO: 0019012; C:violin; IEA.
DR GO: 0003676; F:nucleic acid binding; IEA.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00098; Znf_CCHC; 1.
DR PRINTS: PR00939; C2HCZNFINGER.
DR SMART: SM00343; Znf_CCHC; 1.
DR PROSITE: PS50158; Znf_CCHC; 1.
KM Core protein; Polyprotein.
FT NON_TER 1
FT SEQUENCE 91 AA; 10233 MW; 30031F286DD006B1 CRC64;
SQ

Query Match 84.1%; Score 37; DB 15; Length 91;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
Db 45 EPSAPPEE 52

RESULT 23

Q9DYQ4 PRELIMINARY; PRT; 94 AA.

ID Q9DYQ4
AC Q9DYQ4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gag polyprotein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461476; PubMed=11005867;
RA Martinez-Picado J., DePaquale M.P., Karleous N., Hanna G.J.,
RA Wong J., Finzi D., Rosenberg E., Gunthard H.F., Sutton L., Savara A.,
RA Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,
RA Sillitani R., D'Agostino R.T.;
RT "Antiretroviral resistance during successful therapy of HIV type 1
infection.";
RT Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).
RL EMBL: AF292888; AAG25536.1; -.
DR HSSP: P05888; IAAF.
DR GO: 0019012; C:violin; IEA.
DR GO: 0003676; F:nucleic acid binding; IEA.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00098; Znf_CCHC; 1.
DR PRINTS: PR00939; C2HCZNFINGER.
DR SMART: SM00343; Znf_CCHC; 1.
DR PROSITE: PS50158; Znf_CCHC; 1.
KM Core protein; Polyprotein.
FT NON_TER 1
FT SEQUENCE 94 AA; 10642 MW; FDBF29CE3464BB8E CRC64;
SQ

Query Match 84.1%; Score 37; DB 15; Length 94;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
:|||||
Db 48 EPSAPPEE 55

RESULT 24
09DY01 PRELIMINARY; PRT; 94 AA.

AC 09DY01; 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE 01-OCT-2003 (TREMblrel. 25, Last annotation update)
GN Gag polyprotein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirda; Retrovirdae; Lentivirus.
NCBI_TaxID=11676;
RN [1] SEQUENCE FROM N.A.
RX MEDLINE=20461476; PubMed=11005867;
RA Martinez-Picado J., DePaquale M.P., Kartsonis N., Hanna G.J.,
Wong J., Finzi D., Rosenberg E., Gunthard H.F., Sutton L., Savara A.,
Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,
Siliciano R., D'Aquila R.T.;
RT "Antiretroviral resistance during successful therapy of HIV type 1
infection";
RL Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).
DR EMBL; AF292890; AAG2553.1; -.
DR HSSP; P05888; 1AUF.
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_CCHC; 1.
DR PROSITE; PS50158; ZF_CCHC; 1.
KW Core protein; Polyprotein.
FT NON_TER 1 1
SQ SEQUENCE 94 AA; 10659 MW; 42EAB775ED726C7 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 94;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
:|||||
Db 48 EPSAPPEE 55

RESULT 25
09DY07 PRELIMINARY; PRT; 94 AA.

AC 09DY07; 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DE 01-OCT-2003 (TREMblrel. 25, Last annotation update)
GN Gag polyprotein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirda; Retrovirdae; Lentivirus.
NCBI_TaxID=11676;
RN [1] SEQUENCE FROM N.A.
RX MEDLINE=20461476; PubMed=11005867;
RA Martinez-Picado J., DePaquale M.P., Kartsonis N., Hanna G.J.,
Wong J., Finzi D., Rosenberg E., Gunthard H.F., Sutton L., Savara A.,
Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,
Siliciano R., D'Aquila R.T.;
RT "Antiretroviral resistance during successful therapy of HIV type 1
infection";
RL Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).
DR EMBL; AF292886; AAG2553.1; -.
DR HSSP; P05888; 1AUF.

DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; ZF_CCHC; 1.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_CCHC; 1.
DR PROSITE; PS50158; ZF_CCHC; 1.
KW Core protein; Polyprotein.
FT NON_TER 1 1
SQ SEQUENCE 94 AA; 10586 MW; 2997A0CE5ED73236 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 94;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
:|||||
Db 48 EPSAPPEE 55

RESULT 26
038202 PRELIMINARY; PRT; 95 AA.

AC 038202; 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-OCT-2003 (TREMblrel. 25, Last annotation update)
GN Gag protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirda; Retrovirdae; Lentivirus.
NCBI_TaxID=11676;
RN [1] SEQUENCE FROM N.A.
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imachi H., Imachi T., Lane H.C., Falloon J.,
Vasudevarchi M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
the protease gene and in its Gag substrate cleavage sites";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024099; AAB82975.1; -.
DR HSSP; P05888; 1AUF.
DR GO; GO:0019012; C:virion; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; ZF_CCHC; 2.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_CCHC; 2.
DR PROSITE; PS50158; ZF_CCHC; 1.
KW Core protein; Polyprotein.
FT NON_TER 1 1
SQ SEQUENCE 95 AA; 10631 MW; 01409EB8FEB6D26 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 95;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
:|||||
Db 61 EPSAPPEE 68

RESULT 27
038182 PRELIMINARY; PRT; 95 AA.

AC 038182; 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DE 01-OCT-2003 (TREMblrel. 25, Last annotation update)
GN Gag protein (Fragment).
OS Human immunodeficiency virus 1.

OC viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404676; PubMed=9261388;
 RA Zhang Y.M., Imanishi H., Imanishi T., Lane H.C., Falloon J.,
 Vasudevachari M.B., Salzman N.P.;
 RT "Drug resistance during indinavir therapy is caused by mutations in
 the protease gene and in its Gag substrate cleavage sites.";
 RL J. Virol. 71:6662-6670(1997).
 DR EMBL; AF024079; AAB82955.1; -.
 DR HSPSP; P05888; IAAF.
 DR GO; GO:0019012; C:viral; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf_CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; Znf_C2HC; 2.
 DR PROSITE; PS50158; ZF_CCHC; 1.
 DR Core protein; Polyprotein.
 FT NON TER 1
 FT 95 95
 SQ SEQUENCE 95 AA; 10690 MW; F1E21554E9EB6D3A CRC64;

Query Match 84.1%; Score 37; DB 15; Length 95;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPE 8
 Db 61 EPSAPPPE 68

RESULT 28

038195 PRELIMINARY; PRT; 96 AA.
 AC 038195;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404676; PubMed=9261388;
 RA Zhang Y.M., Imanishi H., Imanishi T., Lane H.C., Falloon J.,
 Vasudevachari M.B., Salzman N.P.;
 RT "Drug resistance during indinavir therapy is caused by mutations in
 the protease gene and in its Gag substrate cleavage sites.";
 RL J. Virol. 71:6662-6670(1997).
 DR EMBL; AF024092; AAB82968.1; -.
 DR HSPSP; P05888; IAAF.
 DR GO; GO:0019012; C:viral; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf_CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; Znf_C2HC; 2.
 DR PROSITE; PS50158; ZF_CCHC; 2.
 DR Core protein; Polyprotein.
 FT NON TER 1
 FT 96 96
 SQ SEQUENCE 96 AA; 10860 MW; C23589A930BCE78 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPE 8
 Db 61 EPSAPPPE 68

Db 62 EPSAPPPE 69

RESULT 29

038214 PRELIMINARY; PRT; 96 AA.
 AC 038214;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404676; PubMed=9261388;
 RA Zhang Y.M., Imanishi H., Imanishi T., Lane H.C., Falloon J.,
 Vasudevachari M.B., Salzman N.P.;
 RT "Drug resistance during indinavir therapy is caused by mutations in
 the protease gene and in its Gag substrate cleavage sites.";
 RL J. Virol. 71:6662-6670(1997).
 DR EMBL; AF024111; AAB82987.1; -.
 DR HSPSP; P05888; IAAF.
 DR GO; GO:0019012; C:viral; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf_CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR PROSITE; PS50158; ZF_CCHC; 2.
 DR Core protein; Polyprotein.
 FT NON TER 1
 FT 96 96
 SQ SEQUENCE 96 AA; 10838 MW; DBE103AA90B8CD78 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPE 8
 Db 62 EPSAPPPE 69

RESULT 30

038215 PRELIMINARY; PRT; 96 AA.
 AC 038215;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404676; PubMed=9261388;
 RA Zhang Y.M., Imanishi H., Imanishi T., Lane H.C., Falloon J.,
 Vasudevachari M.B., Salzman N.P.;
 RT "Drug resistance during indinavir therapy is caused by mutations in
 the protease gene and in its Gag substrate cleavage sites.";
 RL J. Virol. 71:6662-6670(1997).
 DR EMBL; AF024112; AAB82988.1; -.
 DR HSPSP; P05888; IAAF.
 DR GO; GO:0019012; C:viral; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf_CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; Znf_C2HC; 2.

DR PROSITE; PS50158; 2P CCHC; 2.
 KW Core protein; Polyprotein.
 FT NON_TER 1
 SQ SEQUENCE 96 AA; 10910 MW; 79E303AA90BB40CE CRC64;
 Query Match 84.1%; Score 37; DB 15; Length 96;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
 :||:||||
 Db 62 EPSAPPEE 69

RESULT 31
 ID 038208 PRELIMINARY; PRT; 96 AA.
 AC 038208;
 DT 01-JAN-1998 (TEMBLrel. 05, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DE 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NC NCB1_TaxID=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404676; PubMed=9261388;
 RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
 RA Vasudevachari M.B., Salzman N.P.;
 RT "Drug resistance during indinavir therapy is caused by mutations in
 the protease gene and in its Gag substrate cleavage sites.";
 RL J. Virol. 71:6662-6670(1997).
 DR HSBP; AF024105; AAB82981.1; -.
 DR HSBP; P05888; IAAF.
 DR GO; GO:0019012; C:vition; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf_CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR PROSITE; PS50158; ZF_CCHC; 2.
 KW Core protein; Polyprotein.
 FT NON_TER 1
 FT NON_TER 96
 SQ SEQUENCE 96 AA; 10838 MW; DBE103AA90B8CD78 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
 :||:||||
 Db 62 EPSAPPEE 69

RESULT 32
 ID 038218 PRELIMINARY; PRT; 96 AA.
 AC 038218;
 DT 01-JAN-1998 (TEMBLrel. 05, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DE 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NC NCB1_TaxID=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404676; PubMed=9261388;
 RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
 RA Vasudevachari M.B., Salzman N.P.;
 RT "Drug resistance during indinavir therapy is caused by mutations in
 the protease gene and in its Gag substrate cleavage sites.";
 RL J. Virol. 71:6662-6670(1997).
 DR HSBP; AF024107; AAB82983.1; -.
 DR HSBP; P05888; IAAF.
 DR GO; GO:0019012; C:vition; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf_CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; Znf_CCHC; 2.
 DR PROSITE; PS50158; ZF_CCHC; 2.
 KW Core protein; Polyprotein.
 FT NON_TER 1
 FT NON_TER 96
 SQ SEQUENCE 96 AA; 10817 MW; 330C03AA90A4C6FB CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
 :||:||||
 Db 62 EPSAPPEE 69

RESULT 34
 ID 038193 PRELIMINARY; PRT; 96 AA.
 AC 038193;

RA Vasudevachari M.B., Salzman N.P.;
 RT "Drug resistance during indinavir therapy is caused by mutations in
 the protease gene and in its Gag substrate cleavage sites.";
 RL J. Virol. 71:6662-6670(1997).
 DR EMBL; AF024115; AAB82991.1; -.
 DR HSBP; P05888; IAAF.
 DR GO; GO:0019012; C:vition; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf_CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR PROSITE; PS50158; ZF_CCHC; 2.
 KW Core protein; Polyprotein.
 FT NON_TER 1
 FT NON_TER 96
 SQ SEQUENCE 96 AA; 10838 MW; DBE103AA90B8CD78 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
 :||:||||
 Db 62 EPSAPPEE 69

RESULT 33
 ID 038210 PRELIMINARY; PRT; 96 AA.
 AC 038210;
 DT 01-JAN-1998 (TEMBLrel. 05, Created)
 DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
 DE 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NC NCB1_TaxID=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404676; PubMed=9261388;
 RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
 RA Vasudevachari M.B., Salzman N.P.;
 RT "Drug resistance during indinavir therapy is caused by mutations in
 the protease gene and in its Gag substrate cleavage sites.";
 RL J. Virol. 71:6662-6670(1997).
 DR EMBL; AF024107; AAB82983.1; -.
 DR HSBP; P05888; IAAF.
 DR GO; GO:0019012; C:vition; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf_CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; Znf_CCHC; 2.
 DR PROSITE; PS50158; ZF_CCHC; 2.
 KW Core protein; Polyprotein.
 FT NON_TER 1
 FT NON_TER 96
 SQ SEQUENCE 96 AA; 10817 MW; 330C03AA90A4C6FB CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
 :||:||||
 Db 62 EPSAPPEE 69

RESULT 34
 ID 038193 PRELIMINARY; PRT; 96 AA.
 AC 038193;

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DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).
GN
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imanichi H., Imanichi T., Lane H.C., Falloon J.,
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024090; AAB82966.1; -.
DR HSSP; P05888; 1AAF.
DR GO; GO:0019012; C:viral; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf_CCHC; 2.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_CCHC; 2.
DR PROSITE; PS50158; ZF_CCHC; 2.
DR Core protein; Polyprotein.
FT NON TER 1
FT 96
SQ SEQUENCE 96 AA; 10778 MW; 328FA21B20B8CD64 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPE 8
Db 62 EPSAPPE 69

RESULT 35
038183 PRELIMINARY; PRT; 96 AA.
ID 038183;
AC 038183;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).
GN
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imanichi H., Imanichi T., Lane H.C., Falloon J.,
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024080; AAB82966.1; -.
DR HSSP; P05888; 1AAF.
DR GO; GO:0019012; C:viral; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf_CCHC; 2.
DR PRINTS; PR00939; C2HCZNFINGER.
DR SMART; SM00343; Znf_CCHC; 2.
DR PROSITE; PS50158; ZF_CCHC; 2.
DR Core protein; Polyprotein.
FT NON TER 1
FT 96
SQ SEQUENCE 96 AA; 10778 MW; 328FA21B20B8CD64 CRC64;

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Query Match 84.1%; Score 37; DB 15; Length 96;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPE 8
Db 62 EPSAPPE 69

RESULT 36
038204 PRELIMINARY; PRT; 96 AA.
ID 038204;
AC 038204;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).
GN
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imanichi H., Imanichi T., Lane H.C., Falloon J.,
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024101; AAB82977.1; -.
DR HSSP; P05888; 1AAF.
DR GO; GO:0019012; C:viral; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00098; zf_CCHC; 2.
DR PRINTS; PR00939; C2HCZNFINGER.
DR PROSITE; PS50158; ZF_CCHC; 2.
DR Core protein; Polyprotein.
FT NON TER 1
FT 96
SQ SEQUENCE 96 AA; 10893 MW; 5A708AAA90A82376 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPE 8
Db 62 EPSAPPE 69

RESULT 37
038221 PRELIMINARY; PRT; 96 AA.
ID 038221;
AC 038221;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).
GN
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imanichi H., Imanichi T., Lane H.C., Falloon J.,
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL; AF024118; AAB82994.1; -.
DR HSSP; P05888; 1AAF.

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DR GO:0019012; C.vitron; IEA.
DR GO:0003676; F.nucleic acid binding; IEA.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00098; Zf-CCHC; 2.
DR PRINTS; PRO0939; C2HCZNFINGER.
DR SMART; SM00343; Znf_CCHC; 2.
DR PROSITE; PS50158; Zf_CCHC; 2.
KW Core protein; Polypeptide.
FT NON_TER 1 1
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 10894 MW; D46A82B208B15CF1 CRC64;
Query Match 84.1%; Score 37; DB 15; Length 96;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSSPPEE 8
DB 62 EPSAPPPEE 69
RESULT 38
ID 038205 PRELIMINARY; PRT; 96 AA.
AC 038205;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JUN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
the protease gene and in its gag substrate cleavage sites.";
RT J. Virol. 71:6662-6670(1997).
RL EMBL; AF024102; AAB82978.1; -.
DR HSSP; P05888; IAAF.
DR GO:0019012; C.vitron; IEA.
DR GO:0003676; F.nucleic acid binding; IEA.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam; PF00098; Zf-CCHC; 2.
DR PRINTS; PRO0939; C2HCZNFINGER.
DR PROSITE; PS50158; Zf_CCHC; 2.
KW Core protein; Polypeptide.
FT NON_TER 1 1
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 10778 MW; 328FA21B20B8CD64 CRC64;
Query Match 84.1%; Score 37; DB 15; Length 96;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSSPPEE 8
DB 62 EPSAPPPEE 69
RESULT 39
ID 038206 PRELIMINARY; PRT; 96 AA.
AC 038206;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JUN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
the protease gene and in its gag substrate cleavage sites.";
RT J. Virol. 71:6662-6670(1997).
RL EMBL; AF024103; AAB82979.1; -.
DR HSSP; P05888; IAAF.
DR GO:0019012; C.vitron; IEA.
DR GO:0003676; F.nucleic acid binding; IEA.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam; PF00098; Zf-CCHC; 2.
DR PRINTS; PRO0939; C2HCZNFINGER.
DR SMART; SM00343; Znf_CCHC; 2.
DR PROSITE; PS50158; Zf_CCHC; 2.
KW Core protein; Polypeptide.
FT NON_TER 1 1
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 10838 MW; DBE103AA90B8CD78 CRC64;
Query Match 84.1%; Score 37; DB 15; Length 96;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSSPPEE 8
DB 62 EPSAPPPEE 69
RESULT 40
ID 038198 PRELIMINARY; PRT; 96 AA.
AC 038198;
DT 01-JAN-1998 (TEMBLrel. 05, Created)
DT 01-JUN-1998 (TEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
the protease gene and in its gag substrate cleavage sites.";
RT J. Virol. 71:6662-6670(1997).
RL EMBL; AF024095; AAB82971.1; -.
DR HSSP; P05888; IAAF.
DR GO:0019012; C.vitron; IEA.
DR GO:0003676; F.nucleic acid binding; IEA.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam; PF00098; Zf-CCHC; 2.
DR PRINTS; PRO0939; C2HCZNFINGER.
DR PROSITE; PS50158; Zf_CCHC; 2.
KW Core protein; Polypeptide.
FT NON_TER 1 1
FT NON_TER 96 96
SQ SEQUENCE 96 AA; 10810 MW; F6C269BE6748CD66 CRC64;
Query Match 84.1%; Score 37; DB 15; Length 96;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSSPPEE 8
DB 62 EPSAPPPEE 69

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RESULT 41
038207 PRELIMINARY; PRT; 96 AA.
AC 038207;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imanichi H., Imanichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL: AF024104; AAB82980.1; -.
DR HSSP: P05888; 1AAF.
DR GO: GO:0019012; C:virion; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00098; zf-CCHC; 2.
DR PRINTS: PR00939; C2HCZNFINGER.
DR SMART: SM00343; Znf_CCHC; 2.
DR PROSITE: PS50158; ZF_CCHC; 2.
DR Core protein; Polyprotein.
FT NON TER 1
FT NON TER 96
SQ SEQUENCE 96 AA; 10778 MW; FD3A7FCA90B8CD65 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPE 8
Db 62 EPSAPPE 69

RESULT 42
038197 PRELIMINARY; PRT; 96 AA.
AC 038197;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imanichi H., Imanichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL: AF024094; AAB82970.1; -.
DR HSSP: P05888; 1AAF.
DR GO: GO:0019012; C:virion; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00098; zf-CCHC; 2.
DR PRINTS: PR00939; C2HCZNFINGER.
DR SMART: SM00343; Znf_CCHC; 2.
DR PROSITE: PS50158; ZF_CCHC; 1.
DR Core protein; Polyprotein.
FT NON TER 1
FT NON TER 96
SQ SEQUENCE 96 AA; 10778 MW; FD3A7FCA90B8CD65 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPE 8
Db 62 EPSAPPE 69

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DR PROSITE: PS50158; ZF_CCHC; 2.
KW Core protein; Polyprotein.
FT NON TER 1
FT NON TER 96
SQ SEQUENCE 96 AA; 10810 MW; F6C269BE6748CD66 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPE 8
Db 62 EPSAPPE 69

RESULT 43
038184 PRELIMINARY; PRT; 96 AA.
AC 038184;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP MEDLINE=97404676; PubMed=9261388;
RA Zhang Y.M., Imanichi H., Imanichi T., Lane H.C., Falloon J.,
RA Vasudevachari M.B., Salzman N.P.;
RT "Drug resistance during indinavir therapy is caused by mutations in
RT the protease gene and in its Gag substrate cleavage sites.";
RL J. Virol. 71:6662-6670(1997).
DR EMBL: AF024081; AAB82957.1; -.
DR HSSP: P05888; 1AAF.
DR GO: GO:0019012; C:virion; IEA.
DR GO: GO:0003676; F:nucleic acid binding; IEA.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF00098; zf-CCHC; 1.
DR PRINTS: PR00939; C2HCZNFINGER.
DR SMART: SM00343; Znf_CCHC; 1.
DR PROSITE: PS50158; ZF_CCHC; 1.
DR Core protein; Polyprotein.
FT NON TER 1
FT NON TER 96
SQ SEQUENCE 96 AA; 10861 MW; 5F4E7E1AE0AD9971 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPE 8
Db 62 EPSAPPE 69

RESULT 44
038194 PRELIMINARY; PRT; 96 AA.
AC 038194;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP MEDLINE=97404676; PubMed=9261388;

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RA	Zhang Y.M., Imanishi H., Imanishi T., Lane H.C., Falloon J.,
RT	Vandevachari M.B., Salzman N.P.;
RT	"Drug resistance during indinavir therapy is caused by mutations in
RL	J. Virol. 71:6662-6670(1997)."
DR	HSPB; AF024091; AAB82967.1; -.
DR	GO; GO:0019012; C:viralon; IEA.
DR	InterPro; IPR018781; Znf_CCHC.
DR	Pfam; PF00098; zf-CCHC; 2.
DR	PRINTS; PR00939; C2HCZNFINGER.
DR	PROSITE; PS50158; ZF_CCHC; 2.
KW	Core protein; Polypeptide.
FT	NON_TER 1
FT	NON_TER 1
SQ	SEQUENCE 96 AA; 10778 MW; 328FA21B20B8CD64 CRC64;
QY	Query Match 84.1%; Score 37; DB 15; Length 96; Best Local Similarity 75.0%; Pred.No.32; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Dd	1 KPSSPPEE 8 ::: 62 EPSAPPEE 69
RESULT 45	
ID	038200 PRELIMINARY; PRT; 96 AA.
AC	038200;
DT	01-JAN-1998 (TRENBLrel. 05. Created)
DT	01-JAN-1998 (TRENBLrel. 05. Last sequence update)
DT	01-OCT-2003 (TRENBLrel. 25. Last annotation update)
DB	Gag protein (Fragment).
GN	GAG.
OS	Human immunodeficiency virus 1.
OC	Retroviridae; Retrovirus.
OX	NCBI_TaxID=11676;
RP	SEQUENCE FROM N.A. [1]
RX	MEDLINE=97404676; PubMed=9261388;
RA	Zhang Y.M., Imanishi H., Imanishi T., Lane H.C., Falloon J.,
RT	Vandevachari M.B., Salzman N.P.;
RT	"Drug resistance during indinavir therapy is caused by mutations in
RL	J. Virol. 71:6662-6670(1997)."
DR	HSPB; AF024097; AAB82973.1; -.
DR	GO; GO:0019012; C:viralon; IEA.
DR	InterPro; IPR018781; Znf_CCHC.
DR	Pfam; PF00098; zf-CCHC; 2.
DR	PRINTS; PR00939; C2HCZNFINGER.
DR	SMART; SM00343; ZNF_C2HC; 2.
DR	PROSITE; PS50158; ZF_CCHC; 2.
KW	Core protein; Polypeptide.
FT	NON_TER 1
FT	NON_TER 1
SQ	SEQUENCE 96 AA; 10790 MW; 32958B1B20B8CD64 CRC64;
QY	Query Match 84.1%; Score 37; DB 15; Length 96; Best Local Similarity 75.0%; Pred.No.32; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Dd	1 KPSSPPEE 8 ::: 62 EPSAPPEE 69
RESULT 46	
ID	038211 PRELIMINARY; PRT; 96 AA.

DT	038211;	01-JAN-1998	(TREMBLrel. 05, Created)
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	
DE	Gag protein (Fragment).		
GN	GAG.		
OS	Human immunodeficiency virus 1.		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID=11676;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97404676; PubMed=9261388;		
RA	Zhang Y.M., Imanishi H., Imanishi T., Lane H.C., Falloon J.,		
RA	Vaudevachari M.B., Salzman N.P.;		
RT	"Drug resistance during indinavir therapy is caused by mutations in the protease gene and in its Gag substrate cleavage sites.";		
RL	J. Virol. 71:6662-6670(1997).		
DR	EMBL; AF024108; AAB82984.1; -.		
DR	HSSP; P05888; IAAF.		
DR	GO; GO:0019012; C:virion; IEA.		
DR	GO; GO:003676; F:nucleic acid binding; IEA.		
DR	InterPro; IPR001878; Znf CCHC.		
DR	InterPro; IPR001878; Znf CCHC.		
DR	Pfam; PF00098; zf-CCHC; 2.		
DR	PRINTS; PR00939; C2HCZNFINGER.		
DR	PROSITE; PS50158; ZF CCHC; 2.		
KW	Core protein; Polypotein.		
FT	NON_TER	1	
FT	NON_TER	96	
SO	SEQUENCE	96 AA; 10838 MW; DBE103AA90B8CD78 CRC64;	
QY	Query Match	84.1%; Score 37; DB 15; Length 96;	
Db	Best Local Similarity	75.0%; Pred.No. 32;	
	Matches	6; Conservative	2; Mismatches
		0; Indels	0; Gaps
			0;
	1 KPSSPPER 8		
	:-:-:-:-:-		
	62 EPSAPPER 69		
RESULT 47			
038181			
ID	038181	PRELIMINARY;	PRT; 96 AA.
AC	038181;		
DT	01-JAN-1998	(TREMBLrel. 05, Created)	
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)	
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)	
DE	Gag protein (Fragment).		
GN	GAG.		
OS	Human immunodeficiency virus 1.		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxID=11676;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97404676; PubMed=9261388;		
RA	Zhang Y.M., Imanishi H., Imanishi T., Lane H.C., Falloon J.,		
RA	Vaudevachari M.B., Salzman N.P.;		
RT	"Drug resistance during indinavir therapy is caused by mutations in the protease gene and in its Gag substrate cleavage sites.";		
RL	J. Virol. 71:6662-6670(1997).		
DR	EMBL; AF024078; AAB82954.1; -.		
DR	HSSP; P05888; IAAF.		
DR	GO; GO:0019012; C:virion; IEA.		
DR	GO; GO:003676; F:nucleic acid binding; IEA.		
DR	InterPro; IPR001878; Znf CCHC.		
DR	Pfam; PF00098; zf-CCHC; 2.		
DR	PRINTS; PR00939; C2HCZNFINGER.		
DR	SMART; SM00343; Znf CCHC; 2.		
DR	PROSITE; PS50158; ZF CCHC; 2.		
KW	Core protein; Polypotein.		
FT	NON_TER	1	
FT	NON_TER	96	
SO	SEQUENCE	96 AA; 10810 MW; EEA6E10FD748CD67 CRC64;	

Query Match 84.1%; Score 37; DB 15; Length 96;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
 DB 62 EPSAPPE 69

RESULT 48

038216 PRELIMINARY; PRT; 96 AA.
 AC 038216;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 ON NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404676; PubMed=9261388;
 RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
 RT "Drug resistance during indinavir therapy is caused by mutations in
 the protease gene and in its Gag substrate cleavage sites.";
 RL J. Virol. 71:6662-6670(1997).
 DR EMBL; AF024113; AAB82989.1; -.
 DR HSSP; P05888; IAAF.
 DR GO; GO:0019012; C:virion; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf_CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR PROSITE; PS50158; ZF_CCHC; 2.
 KW Core protein; Polyprotein.
 FT NON_TER 1
 FT NON_TER 96
 SQ SEQUENCE 96 AA; 10838 MW; DBE103AA90B8CD78 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
 DB 62 EPSAPPE 69

RESULT 49

038213 PRELIMINARY; PRT; 96 AA.
 AC 038213;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 ON NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404676; PubMed=9261388;
 RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
 RT "Drug resistance during indinavir therapy is caused by mutations in
 the protease gene and in its Gag substrate cleavage sites.";
 RL J. Virol. 71:6662-6670(1997).
 DR EMBL; AF024110; AAB82986.1; -.
 DR HSSP; P05888; IAAF.

DR GO; GO:0019012; C:virion; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf_CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR PROSITE; PS50158; ZF_CCHC; 2.
 KW Core protein; Polyprotein.
 FT NON_TER 1
 FT NON_TER 96
 SQ SEQUENCE 96 AA; 10838 MW; DBE103AA90B8CD78 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
 DB 62 EPSAPPE 69

RESULT 50

038222 PRELIMINARY; PRT; 96 AA.
 AC 038222;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Gag protein (Fragment).
 GN GAG.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 ON NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97404676; PubMed=9261388;
 RA Zhang Y.M., Imamichi H., Imamichi T., Lane H.C., Falloon J.,
 RT "Drug resistance during indinavir therapy is caused by mutations in
 the protease gene and in its Gag substrate cleavage sites.";
 RL J. Virol. 71:6662-6670(1997).
 DR EMBL; AF024119; AAB82995.1; -.
 DR HSSP; P05888; IAAF.
 DR GO; GO:0019012; C:virion; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00098; zf_CCHC; 2.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; ZNF_CCHC; 2.
 DR PROSITE; PS50158; ZF_CCHC; 2.
 KW Core protein; Polyprotein.
 FT NON_TER 1
 FT NON_TER 96
 SQ SEQUENCE 96 AA; 10852 MW; C23EB2AA81AD9C78 CRC64;

Query Match 84.1%; Score 37; DB 15; Length 96;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
 DB 62 EPSAPPE 69

Search completed: June 18, 2004, 12:59:58
 Job time : 52 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model1

Run on: June 18, 2004, 12:56:24 ; Search time 22 Seconds
(without alignments)
34.979 Million cell updates/sec

Title: US-10-655-201-2

Perfect score: 44

Sequence: 1 KPSPPEE 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	100.0	431	1 UKHU	u-plasminogen acti
2	44	100.0	433	1 UKBAV	u-plasminogen acti
3	39	88.6	990	2 A86215	protein T6D22.8 [l
4	36	81.8	124	2 H87616	cytochrome c famil
5	36	81.8	261	2 C87204	thioesterase [impo
6	36	81.8	418	2 A47281	pigment epithelial
7	36	81.8	880	2 T02245	hypothetical prote
8	36	81.8	1185	2 T46428	hypothetical prote
9	36	81.8	1358	2 A29360	SIR4 protein - yea
10	36	81.8	1806	1 CGH1E	collagen alpha 1(X
11	35	79.5	90	2 B83542	hypothetical prote
12	35	79.5	216	2 T26841	hypothetical prote
13	35	79.5	249	2 H72858	apoptosis inhibito
14	35	79.5	249	2 T41814	IAP2 orf171 - Bomby
15	35	79.5	374	2 T07887	G box-binding prot
16	35	79.5	376	2 T07882	mRNA 3'-end proces
17	35	79.5	407	2 D69316	protein-tyrosine-p
18	35	79.5	440	2 T50213	hypothetical prote
19	35	79.5	516	2 E96583	hypothetical prote
20	35	79.5	754	1 BABOH	peptide-aspartate
21	35	79.5	765	2 A53047	6-phosphofructokin
22	35	79.5	784	2 JC2055	6-phosphofructokin
23	35	79.5	791	2 A53206	6-phosphofructokin
24	35	79.5	1179	2 G75459	DNA-directed RNA p
25	35	79.5	1186	2 T12737	tail protein - Met
26	35	79.5	1240	1 DJB821	DNA-directed DNA p
27	35	79.5	1691	1 D54689	protein-tyrosine-p
28	35	79.5	1863	2 S46217	protein-tyrosine-p
29	35	79.5	1894	2 C54689	protein-tyrosine-p

30	35	79.5	1907	2 S50893	protein-tyrosine-p
31	35	79.5	1912	2 A56178	protein-tyrosine-p
32	35	79.5	2265	1 FNBO	fibronectin - bovi
33	35	79.5	2386	1 FNHU	fibronectin precu
34	35	79.5	2477	2 S14428	fibronectin precu
35	34	77.3	66	2 AG2522	hypothetical prote
36	34	77.3	122	2 F83167	hypothetical prote
37	34	77.3	124	2 H82468	hypothetical prote
38	34	77.3	136	2 E72759	hypothetical prote
39	34	77.3	140	2 E72505	hypothetical prote
40	34	77.3	173	2 T31243	hypothetical prote
41	34	77.3	231	2 H82155	hypothetical prote
42	34	77.3	301	2 A60548	synaptophysin - Pa
43	34	77.3	310	2 T33972	hypothetical prote
44	34	77.3	382	2 G84900	G-box binding bzp
45	34	77.3	458	2 UC7868	triacylglycerol 11
46	34	77.3	462	2 A42401	macrophage elastas
47	34	77.3	500	1 FOWMLV	gag polyprotein -
48	34	77.3	500	1 FOWMH4	gag polyprotein -
49	34	77.3	500	2 S33979	gag polyprotein -
50	34	77.3	502	1 FOWMA2	gag polyprotein -
51	34	77.3	506	1 A38068	gag polyprotein -
52	34	77.3	512	1 FOWMH3	gag polyprotein -
53	34	77.3	544	2 S75109	cytochrome-c oxida
54	34	77.3	553	1 A42499	mullerian inhibiti
55	34	77.3	555	1 S20100	mullerian inhibiti
56	34	77.3	558	2 A46225	nuclear orphan rec
57	34	77.3	558	2 A57040	nuclear orphan rec
58	34	77.3	559	2 I84692	nuclear orphan rec
59	34	77.3	615	2 T41576	hypothetical prote
60	34	77.3	711	2 T04455	hypothetical prote
61	34	77.3	760	2 F86387	probable pro kinas
62	34	77.3	795	2 T49835	hypothetical prote
63	34	77.3	825	2 F75508	conserved hypothec
64	34	77.3	826	2 H84683	hypothetical prote
65	34	77.3	866	2 A54442	3',5'-cyclic-nucle
66	34	77.3	928	2 S64350	hypothetical prote
67	34	77.3	1071	2 E85343	hypothetical prote
68	34	77.3	1488	2 T02856	probable membrane
69	34	77.3	1571	2 T00062	hypothetical prote
70	34	77.3	2023	2 T13154	polycomb protein e
71	34	77.3	3938	2 T42761	Bassoon protein -
72	34	77.3	3942	2 T42730	Bassoon protein -
73	34	77.3	7962	2 I38346	elastic titin - hu
74	33	75.0	133	2 B70338	general secretion
75	33	75.0	137	2 H70547	hypothetical prote
76	33	75.0	153	2 E47021	pectic enzyme secr
77	33	75.0	176	2 F72651	hypothetical prote
78	33	75.0	245	2 AD2269	hypothetical prote
79	33	75.0	301	2 C64633	hook assembly prot
80	33	75.0	326	2 PC4028	dihydrolipomide S
81	33	75.0	353	2 F71881	probable flagellar
82	33	75.0	366	2 A53286	cell-surface glyco
83	33	75.0	378	1 H69004	2-oxoglutarate-fer
84	33	75.0	393	2 S44202	acyl-lacyl-carrier
85	33	75.0	394	2 C84905	probable extensin
86	33	75.0	399	1 OHSPAD	acyl-lacyl-carrier
87	33	75.0	411	1 E71178	translation initia
88	33	75.0	411	2 F75163	translation initia
89	33	75.0	424	1 H69323	translation initia
90	33	75.0	445	2 AF0033	H+-transporting tw
91	33	75.0	506	1 FOLJG3	gag polyprotein -
92	33	75.0	514	2 A31643	cell adhesion 80K
93	33	75.0	514	2 A44100	cell adhesion mole
94	33	75.0	537	2 T24945	hypothetical prote
95	33	75.0	596	2 G87659	peptidase M3 famil
96	33	75.0	640	1 UZADP7	terminal protein p
97	33	75.0	830	1 B48723	replication licens
98	33	75.0	847	2 F96531	hypothetical prote
99	33	75.0	927	2 B82075	sensor histidine k
100	33	75.0	975	2 T08606	protein phosphatas
101	33	75.0	1014	1 S75023	sensory transducti
102	33	75.0	1264	2 A36858	G2R protein - vari

103	33	75.0	1296	1	HMSOIF	aggregation protei	176	31	70.5	133	2	AE3330	hypothetical prote
104	33	75.0	1305	2	H41662	150K mating aggreg	177	31	70.5	135	2	G72721	hypothetical prote
105	33	75.0	1306	2	S22624	aggregation protei	178	31	70.5	137	2	A75292	hypothetical prote
106	33	75.0	1896	2	B72175	D15R protein - var	179	31	70.5	156	2	D75605	hypothetical prote
107	33	75.0	1897	2	T28621	hypothetical prote	180	31	70.5	157	2	S19735	hypothetical prote
108	33	75.0	4957	2	T03455	ALK protein - huma	181	31	70.5	158	2	UC1095	pre-S protein - du
109	33	75.0	5262	2	T03454	ALK protein - huma	182	31	70.5	160	2	GE0136	lectin precursor -
110	32	72.7	101	2	T36269	probable redoxin -	183	31	70.5	165	2	G84767	glycine decarboxyl
111	32	72.7	115	2	A23925	proline-rich phosph	184	31	70.5	166	2	A86450	probable glycine c
112	32	72.7	138	2	A95913	hypothetical membr	185	31	70.5	179	2	T19557	hypothetical prote
113	32	72.7	170	2	F87236	conserved hypochet	186	31	70.5	187	2	S74987	hypothetical prote
114	32	72.7	174	1	RDSPTA	ferredoxin-chloroed	187	31	70.5	186	2	E75591	hypothetical prote
115	32	72.7	178	2	E84049	hypothetical prote	188	31	70.5	199	2	T27097	hypothetical prote
116	32	72.7	207	2	A56190	vitlin - rat (fragm	189	31	70.5	209	2	T20975	hypothetical prote
117	32	72.7	238	2	T40820	proline-rich prote	190	31	70.5	215	2	T27098	hypothetical prote
118	32	72.7	243	2	A31231	high-affinity IGE	191	31	70.5	232	2	T26209	hypothetical prote
119	32	72.7	247	2	H69030	coenzyme PQQ synth	192	31	70.5	226	2	C96794	hypothetical prote
120	32	72.7	251	2	D31957	tropomycin T, skelet	193	31	70.5	228	1	S35689	venomadin A (EC 3.4
121	32	72.7	253	2	B34327	tropomycin T, fast s	194	31	70.5	229	2	C96013	probable transcript
122	32	72.7	257	2	B31957	tropomycin T, skelet	195	31	70.5	237	2	G65084	hypothetical prote
123	32	72.7	263	2	C31957	tropomycin T, skelet	196	31	70.5	242	2	T27999	hypothetical prote
124	32	72.7	283	2	S13383	hydroxyproline-ric	197	31	70.5	250	2	T03595	L-ascorbate peroxi
125	32	72.7	303	2	S28264	hydroxyproline-ric	198	31	70.5	253	2	F86184	hypothetical prote
126	32	72.7	328	2	UQ0985	hydroxyproline-ric	199	31	70.5	268	2	H84684	En/Spm-like transp
127	32	72.7	332	2	E86448	hydroxyproline-ric	200	31	70.5	269	2	D64668	hypothetical prote
128	32	72.7	350	2	S22456	hydroxyproline-ric	201	31	70.5	277	2	I38857	microtubule-associ
129	32	72.7	359	2	S20500	hydroxyproline-ric	202	31	70.5	280	2	B87305	metallo-beta-lacta
130	32	72.7	384	2	AG3013	conserved hypochet	203	31	70.5	283	2	T51091	hypothetical prote
131	32	72.7	384	2	H98270	hypothetical prote	204	31	70.5	304	2	T44637	dipeptide transpor
132	32	72.7	405	2	T17271	hypothetical prote	205	31	70.5	308	2	I48080	coatomer complex e
133	32	72.7	421	2	S38948	serine-ENNA ligase	206	31	70.5	308	2	I46019	coatomer complex e
134	32	72.7	430	2	AD0138	ToIB colicin import	207	31	70.5	310	2	E84612	homeodomain transc
135	32	72.7	434	2	C71434	probable phosphati	208	31	70.5	311	2	S47136	hypothetical prote
136	32	72.7	436	2	I49714	MHC H-2K/Lt-W5-link	209	31	70.5	312	2	T19675	hypothetical prote
137	32	72.7	517	2	E89530	protein H28G03.2 [210	31	70.5	314	2	T38955	hypothetical prote
138	32	72.7	532	2	JE0091	testis sodium chan	211	31	70.5	314	2	B70013	hypothetical prote
139	32	72.7	539	2	H71280	hypothetical prote	212	31	70.5	316	2	UC6549	apolipoprotein E P
140	32	72.7	549	1	TEBEHC	segment protein -	213	31	70.5	316	2	S26478	apolipoprotein E -
141	32	72.7	556	2	T03114	hypothetical protei	214	31	70.5	316	2	I45996	conserved hypochet
142	32	72.7	556	2	T47552	hypothetical prote	215	31	70.5	317	2	H75297	hypothetical prote
143	32	72.7	562	2	F72771	probable lysyl-tRN	216	31	70.5	318	2	S76295	hypothetical prote
144	32	72.7	592	2	T32402	hypothetical prote	217	31	70.5	322	2	E84105	oligopeptide ABC t
145	32	72.7	613	2	T42671	hypothetical prote	218	31	70.5	323	2	T29032	hypothetical prote
146	32	72.7	615	2	T25245	hypothetical prote	219	31	70.5	329	1	G3M5C	Ig gamma-3 chain C
147	32	72.7	632	2	AF3095	nitric oxide reduc	220	31	70.5	332	2	T10064	cytochrome-induced
148	32	72.7	632	2	D98191	trkA-like protein	221	31	70.5	332	2	D86295	hypothetical prote
149	32	72.7	685	2	T18964	hypothetical prote	222	31	70.5	339	2	T26328	hypothetical prote
150	32	72.7	741	2	A83271	hypothetical prote	223	31	70.5	344	1	SAVAD	large surface anti
151	32	72.7	783	2	T38891	hypothetical prote	224	31	70.5	359	2	AB2733	NADH ubiquinone ox
152	32	72.7	832	2	H72278	alpha-mannosidase-	225	31	70.5	359	2	D97514	complex I 24k chal
153	32	72.7	839	2	F75518	hypothetical prote	226	31	70.5	370	2	T33382	hypothetical prote
154	32	72.7	875	2	T50182	ubiquitin-specific	227	31	70.5	372	2	T31060	hypothetical prote
155	32	72.7	950	2	A82986	adenylate cyclase	228	31	70.5	382	2	A88099	protein F18A12.2 [
156	32	72.7	953	2	T01093	luminal-dependent p	229	31	70.5	387	2	T10793	acyl-lacyl-carrier
157	32	72.7	988	2	T25541	hypothetical prote	230	31	70.5	388	1	G3M5M	Ig gamma-3 chain C
158	32	72.7	1234	2	T30254	jumonji protein -	231	31	70.5	398	2	S23351	acyl-lacyl-carrier
159	32	72.7	1249	2	H71404	hypothetical prote	232	31	70.5	405	2	T42992	cyclin D - Caenorh
160	32	72.7	1294	2	T48349	EN2 protein - Ara	233	31	70.5	405	2	T26678	hypothetical prote
161	32	72.7	2054	2	T46612	multi-poz domain p	234	31	70.5	407	2	B47557	retrovirus-related
162	32	72.7	2701	2	S17796	inositol-trisphosp	235	31	70.5	415	2	S29345	translational elonga
163	31	70.5	66	2	AB2510	hypothetical prote	236	31	70.5	416	2	S48957	hypothetical prote
164	31	70.5	74	2	T47211	ccg-6 protein (imp	237	31	70.5	418	2	D71460	probable membrane
165	31	70.5	77	2	S30873	hypothetical prote	238	31	70.5	444	2	F96838	hypothetical prote
166	31	70.5	78	2	H69790	conserved hypochet	239	31	70.5	445	2	B40970	undulin 2 - human
167	31	70.5	81	2	S35586	high potential iro	240	31	70.5	446	2	A34418	H-2 region II bind
168	31	70.5	83	1	IHKREG	high potential iro	241	31	70.5	448	2	D41727	retinoid X recepto
169	31	70.5	85	1	IHKREV	high potential iro	242	31	70.5	458	2	T16041	hypothetical prote
170	31	70.5	84	1	A01955	Ig kappa-B5 chain	243	31	70.5	468	2	H70427	replicative DNA he
171	31	70.5	97	2	S11755	hypothetical prote	244	31	70.5	474	2	E87650	peptidase, M20/M25
172	31	70.5	99	2	T33486	hypothetical prote	245	31	70.5	476	2	A70477	glutamate synthase
173	31	70.5	101	2	G72155	E17R protein - var	246	31	70.5	476	2	S57963	methyl CPG binding
174	31	70.5	101	2	C36891	E17R protein - var	247	31	70.5	480	1	DEGRA	aromatic-L-amino-a
175	31	70.5	101	2	T28479	hypothetical prote	248	31	70.5	487	2	E70961	hypothetical prote

249	31	70.5	496	2	A41264	glucose transport
250	31	70.5	503	2	T10944	cysteine proteinas
251	31	70.5	511	2	C56849	dopamine receptor-
252	31	70.5	518	2	G86454	CDS protein F9L11.
253	31	70.5	520	2	I84718	RXR-beta1 isoform
254	31	70.5	527	2	A32469	80K protein H prec
255	31	70.5	534	2	JC7912	amino-acid N-acetyl
256	31	70.5	536	2	B84549	probable ubiquitin
257	31	70.5	538	2	T16034	hypothetical prote
258	31	70.5	540	2	AC0063	hypothetical prote
259	31	70.5	551	2	G95176	conserved hypothet
260	31	70.5	551	2	E84106	hypothetical prote
261	31	70.5	551	2	A98043	hypothetical prote
262	31	70.5	576	2	AC2195	hypothetical prote
263	31	70.5	579	2	T24536	hypothetical prote
264	31	70.5	580	2	B70668	probable Acyl-CoA
265	31	70.5	585	2	E70930	hypothetical prote
266	31	70.5	588	2	B70618	probable PE protei
267	31	70.5	601	2	T37738	hypothetical prote
268	31	70.5	611	1	S12566	translation initia
269	31	70.5	637	2	AB2403	ABC transporter At
270	31	70.5	639	2	DB3591	probable ATP-depen
271	31	70.5	656	1	A34890	histidine decarbox
272	31	70.5	657	2	H71422	hypothetical prote
273	31	70.5	679	2	H84516	hypothetical prote
274	31	70.5	682	1	S22700	amphiphysin - chic
275	31	70.5	684	2	T37944	hypothetical prote
276	31	70.5	687	1	PYFFW	white protein - fr
277	31	70.5	695	2	S62400	amphiphysin (clone
278	31	70.5	731	2	T09172	probable calcium-a
279	31	70.5	748	2	T49633	glucan 1,4-alpha-g
280	31	70.5	752	2	T34355	hypothetical prote
281	31	70.5	757	2	I38423	aspartyl beta-hydr
282	31	70.5	763	2	S73178	translation initia
283	31	70.5	766	2	A53501	cyclin F - human
284	31	70.5	802	1	S48529	NAB3 protein - yea
285	31	70.5	834	2	T06055	hypothetical prote
286	31	70.5	834	2	T42702	S-receptor kinase
287	31	70.5	849	1	T05181	serine/chreonine k
288	31	70.5	850	2	T14450	berline/chreonine k
289	31	70.5	857	2	S44883	ZC267.3 protein -
290	31	70.5	858	2	AE2085	ferrichrome-iron r
291	31	70.5	863	2	C88546	protein R107.4 [im
292	31	70.5	867	2	H90524	preprotein translo
293	31	70.5	869	2	T22422	hypothetical prote
294	31	70.5	872	2	S62061	SCDs protein - yea
295	31	70.5	882	2	A39030	androgen-binding p
296	31	70.5	928	1	VGEBRG	glycoprotein gi pr
297	31	70.5	928	2	S50578	hypothetical prote
298	31	70.5	929	2	T52517	hypothetical prote
299	31	70.5	932	1	VGEBRC	glycoprotein gi pr
300	31	70.5	939	2	E82121	peptidase, insulin
301	31	70.5	941	2	A86404	probable protein A
302	31	70.5	1033	2	F81595	hypothetical prote
303	31	70.5	1034	1	A33663	enteropeptidase (E
304	31	70.5	1036	1	A34755	nitrogen regulator
305	31	70.5	1043	2	C87645	Acra/AcrD/AcrF fam
306	31	70.5	1043	2	G86550	hypothetical prote
307	31	70.5	1043	2	G72073	hypothetical prote
308	31	70.5	1046	2	T42720	cytoplasmic linker
309	31	70.5	1080	2	E87586	metal ion efflux R
310	31	70.5	1117	2	T19727	hypothetical prote
311	31	70.5	1123	2	S36846	myosin-binding pro
312	31	70.5	1132	2	S37932	hypothetical prote
313	31	70.5	1137	2	A86335	T20H2.9 protein -
314	31	70.5	1138	2	S24614	myosin-binding pro
315	31	70.5	1186	2	T23327	adenomatus polyo
316	31	70.5	1188	2	S49915	extensin-like prot
317	31	70.5	1188	2	T23330	hypothetical prote
318	31	70.5	1212	2	T00332	hypothetical prote
319	31	70.5	1265	2	T02131	hypothetical prote
320	31	70.5	1274	2	E81779	proline dehydrogen
321	31	70.5	1333	2	T00037	hypothetical prote
322	31	70.5	1325	2	T01037	hypothetical prote
323	31	70.5	1440	1	SYHQT	multifunctional am
324	31	70.5	1445	2	T50508	hypothetical prote
325	31	70.5	1464	2	T07050	hypothetical prote
326	31	70.5	1558	2	C89114	protein C37C3.6a l
327	31	70.5	1558	2	A47371	transcription init
328	31	70.5	2167	2	T34395	hypothetical prote
329	31	70.5	2416	2	T13825	adenomatus polyo
330	31	70.5	2763	1	M2BR22	gene 22 protein -
331	31	70.5	2774	2	A43359	microtubule-associ
332	31	70.5	26926	1	I38344	lctn, cardiac mus
333	30.5	69.3	127	2	AB2800	conserved hypothet
334	30.5	69.3	147	2	D97579	hypothetical prote
335	30.5	69.3	282	2	T26635	hypothetical prote
336	30	68.2	46	2	T46224	hypothetical prote
337	30	68.2	53	2	S31531	ribulose-bisphosph
338	30	68.2	54	2	S52452	ribulose-bisphosph
339	30	68.2	54	2	S31529	ribulose-bisphosph
340	30	68.2	54	2	S31530	ribulose-bisphosph
341	30	68.2	54	2	S31531	ribulose-bisphosph
342	30	68.2	54	2	S31552	ribulose-bisphosph
343	30	68.2	54	2	S31527	ribulose-bisphosph
344	30	68.2	54	2	S31528	ribulose-bisphosph
345	30	68.2	54	2	S31533	ribulose-bisphosph
346	30	68.2	54	2	S31537	ribulose-bisphosph
347	30	68.2	54	2	S31536	ribulose-bisphosph
348	30	68.2	54	2	S32706	ribulose-bisphosph
349	30	68.2	55	2	S31535	ribulose-bisphosph
350	30	68.2	55	2	PQ0795	ribulose-bisphosph
351	30	68.2	55	2	PQ0797	ribulose-bisphosph
352	30	68.2	56	2	S49289	ribulose-bisphosph
353	30	68.2	56	2	S49291	ribulose-bisphosph
354	30	68.2	56	2	S49288	ribulose-bisphosph
355	30	68.2	56	2	S49274	ribulose-bisphosph
356	30	68.2	56	2	S49298	ribulose-bisphosph
357	30	68.2	56	2	S49285	ribulose-bisphosph
358	30	68.2	56	2	S49275	ribulose-bisphosph
359	30	68.2	56	2	S49277	ribulose-bisphosph
360	30	68.2	56	2	S49297	ribulose-bisphosph
361	30	68.2	56	2	S49282	ribulose-bisphosph
362	30	68.2	56	2	S49281	ribulose-bisphosph
363	30	68.2	56	2	S49278	ribulose-bisphosph
364	30	68.2	56	2	S49276	ribulose-bisphosph
365	30	68.2	56	2	S49279	ribulose-bisphosph
366	30	68.2	56	2	S49283	ribulose-bisphosph
367	30	68.2	56	2	S49284	ribulose-bisphosph
368	30	68.2	56	2	S49286	ribulose-bisphosph
369	30	68.2	56	2	S49287	ribulose-bisphosph
370	30	68.2	56	2	S49288	ribulose-bisphosph
371	30	68.2	56	2	S49290	ribulose-bisphosph
372	30	68.2	56	2	S49296	ribulose-bisphosph
373	30	68.2	57	2	S31545	ribulose-bisphosph
374	30	68.2	57	2	S31542	ribulose-bisphosph
375	30	68.2	57	2	S31540	ribulose-bisphosph
376	30	68.2	57	2	S31553	ribulose-bisphosph
377	30	68.2	57	2	S39285	ribulose-bisphosph
378	30	68.2	57	2	S39287	ribulose-bisphosph
379	30	68.2	57	2	S39288	ribulose-bisphosph
380	30	68.2	57	2	S39289	ribulose-bisphosph
381	30	68.2	57	2	S39271	ribulose-bisphosph
382	30	68.2	57	2	S39276	ribulose-bisphosph
383	30	68.2	57	2	S39275	ribulose-bisphosph
384	30	68.2	57	2	S39290	ribulose-bisphosph
385	30	68.2	57	2	S39291	ribulose-bisphosph
386	30	68.2	57	2	S52451	ribulose-bisphosph
387	30	68.2	58	2	S31547	ribulose-bisphosph
388	30	68.2	58	2	S31550	ribulose-bisphosph
389	30	68.2	58	2	S31551	ribulose-bisphosph
390	30	68.2	58	2	S31541	ribulose-bisphosph
391	30	68.2	58	2	S31538	ribulose-bisphosph
392	30	68.2	58	2	S31534	ribulose-bisphosph
393	30	68.2	58	2	S31549	ribulose-bisphosph
394	30	68.2	64	2	S32220	ribulose-bisphosph

395	30	68.2	67	2	C81174	hypothetical prote
396	30	68.2	102	2	B34153	Ig kappa chain V-I
397	30	68.2	112	2	T51569	hypothetical prote
398	30	68.2	116	2	S33810	ribulose-bisphosph
399	30	68.2	119	2	B53482	regulatory protein
400	30	68.2	128	2	D38355	basic proline-rich
401	30	68.2	158	2	UC6056	ubiquitin-protein
402	30	68.2	166	1	PIH05C	salivary proline-r
403	30	68.2	170	2	B25372	salivary proline-r
404	30	68.2	170	2	B55663	oligodendrocyte-sp
405	30	68.2	171	2	A27307	proline-rich phosph
406	30	68.2	179	2	F95417	probable aminoglyc
407	30	68.2	180	2	T15426	hypothetical prote
408	30	68.2	185	2	S76706	hypothetical prote
409	30	68.2	187	2	E86324	protein F14d16.27
410	30	68.2	188	2	TJH0481	basic proline-rich
411	30	68.2	188	2	AF2834	conserved hypochet
412	30	68.2	195	2	B97612	hypothetical prote
413	30	68.2	207	2	T24858	hypothetical prote
414	30	68.2	211	2	S37792	hypothetical prote
415	30	68.2	221	2	G72665	hypothetical prote
416	30	68.2	227	2	E90420	DNA endonuclease I
417	30	68.2	234	1	S76823	hypothetical prote
418	30	68.2	234	2	T30427	probable apoptosis
419	30	68.2	236	2	B85025	hypothetical prote
420	30	68.2	239	2	T03078	conserved hypochet
421	30	68.2	241	2	AD2366	hypothetical prote
422	30	68.2	243	2	E70846	hypothetical prote
423	30	68.2	249	2	T10189	L-ascorbate peroxi
424	30	68.2	250	2	D86214	hypothetical prote
425	30	68.2	250	2	T08071	L-ascorbate peroxi
426	30	68.2	250	2	S43157	L-ascorbate peroxi
427	30	68.2	250	2	T07056	L-ascorbate peroxi
428	30	68.2	250	2	A45116	L-ascorbate peroxi
429	30	68.2	250	2	S49914	L-ascorbate peroxi
430	30	68.2	250	2	JE0232	L-ascorbate peroxi
431	30	68.2	251	1	PIH05F	salivary proline-r
432	30	68.2	254	2	G72200	L-phosphoserine
433	30	68.2	263	2	S20866	L-ascorbate peroxi
434	30	68.2	268	2	T15169	hypothetical prote
435	30	68.2	269	2	T24637	hypothetical prote
436	30	68.2	273	2	C88429	protein ceh-43 [im
437	30	68.2	281	2	I38707	fas ligand - human
438	30	68.2	282	2	S43577	C28A5.4 protein (c
439	30	68.2	285	1	I46207	thioredoxin - dog
440	30	68.2	285	1	C97279	thioredoxin reduct
441	30	68.2	290	2	AC2030	hypothetical prote
442	30	68.2	293	2	D90456	oxydoreductase, pr
443	30	68.2	297	2	J01205	attachment protein
444	30	68.2	297	2	J01204	attachment protein
445	30	68.2	298	1	MGNZ	major surface glyc
446	30	68.2	298	1	MGNZRL	major surface glyc
447	30	68.2	304	2	T48281	hypothetical prote
448	30	68.2	309	2	T29293	hypothetical prote
449	30	68.2	310	1	PIH05D	salivary proline-r
450	30	68.2	311	2	E81703	phospholipase D fa
451	30	68.2	315	2	EJ0397	DNA-directed RNA p
452	30	68.2	318	2	JC1171	muscle regulatory
453	30	68.2	322	2	S25299	extensin precursor
454	30	68.2	323	1	GHRB	ig gamma chain C r
455	30	68.2	331	2	C87385	conserved hypochet
456	30	68.2	346	1	BYECPR	phosphatase-repressi
457	30	68.2	346	1	AB0956	periplasmic phosph
458	30	68.2	347	2	S36980	hypothetical prote
459	30	68.2	349	1	QOBE05	HHRF5 protein - hu
460	30	68.2	350	2	I38403	neu differentiation
461	30	68.2	350	2	T04097	acyl-[acyl]-carrier
462	30	68.2	352	1	PIH05B	salivary proline-r
463	30	68.2	362	2	T14172	acyl-[acyl]-carrier
464	30	68.2	366	2	T14264	acyl-[acyl]-carrier
465	30	68.2	396	2	T14268	acyl-[acyl]-carrier
466	30	68.2	399	2	S24995	acyl-[acyl]-carrier
467	30	68.2	401	2	E84869	stearyl-ACP desat

468	30	68.2	401	2	T02958	ribulose-bisphosph
469	30	68.2	402	2	A40678	T-cell adhesion re
470	30	68.2	404	2	S68409	potassium channel
471	30	68.2	406	2	T44819	dolichyl-phosphate
472	30	68.2	407	2	S71264	acyl-[acyl]-carrier
473	30	68.2	411	2	T07806	acyl-[acyl]-carrier
474	30	68.2	411	2	C36793	hypothetical prote
475	30	68.2	413	2	AD2743	conserved hypochet
476	30	68.2	416	2	G97524	hypothetical prote
477	30	68.2	424	2	E83442	probable MFS trans
478	30	68.2	426	1	RKH1LC	ribulose-bisphosph
479	30	68.2	427	1	GQHN	nerve growth facto
480	30	68.2	427	1	A13490	membrane-bound 1yt
481	30	68.2	431	2	T01557	hypothetical prote
482	30	68.2	443	1	I38239	transcription fact
483	30	68.2	448	2	F81703	phospholipase D fa
484	30	68.2	450	1	G72039	2-amino-4-hydroxy-
485	30	68.2	450	2	D86585	dihydropterolate by
486	30	68.2	452	2	S47228	ribulose-bisphosph
487	30	68.2	452	2	S47229	ribulose-bisphosph
488	30	68.2	452	2	S47230	ribulose-bisphosph
489	30	68.2	452	2	S47231	ribulose-bisphosph
490	30	68.2	452	2	S47232	ribulose-bisphosph
491	30	68.2	452	2	S47233	ribulose-bisphosph
492	30	68.2	452	2	S47234	ribulose-bisphosph
493	30	68.2	452	2	S47235	ribulose-bisphosph
494	30	68.2	452	2	S47236	ribulose-bisphosph
495	30	68.2	452	2	S47237	ribulose-bisphosph
496	30	68.2	452	2	S47238	ribulose-bisphosph
497	30	68.2	452	2	S47221	ribulose-bisphosph
498	30	68.2	452	2	S47222	ribulose-bisphosph
499	30	68.2	452	2	S47223	ribulose-bisphosph
500	30	68.2	452	2	S47224	ribulose-bisphosph

ALIGNMENTS

RESULT 1

UKHU

u-Plasminogen activator (BC 3.4.21.73) precursor [validated] - human

N;Alternate names: cellular plasminogen activator; urokinase; urokinase-type plasminogen

N;Content: urokinase-type plasminogen activator chain A; urokinase-type plasminogen acti

in form

C;Species: Homo sapiens (man)

C;Date: 17-Dec-1982 #sequence revision 04-Dec-1986 #ext change 15-Sep-2000

C;Accession: A00931; 152209; J0102; A37561; I38102; S65783; A37563; A37564; A356

R;Riccio, A.; Grimaldi, G.; Verde, P.; Sebastio, G.; Boast, S.; Blasi, F.

Nucleic Acids Res. 13, 2759-2771, 1985

A;Title: The human urokinase-Plasminogen activator gene and its promoter.

A;Reference number: A00931; PMID:85215647; PMID:2387867

A;Accession: A00931

A;Molecule type: DNA

A;Residues: 1431 <R1C>

A;Cross-references: GB:X02419; NID:G37601; PIDN:CAA26268.1; PID:G1834524

A;Note: the authors translated the codon ATG for residue 214 as Ile

R;Nagamine, Y.; Pearson, D.; Gratian, M.

Biochem. Biophys. Res. Commun. 132, 563-569, 1985

A;Title: Exon-intron boundary sliding in the generation of two mRNAs coding for porcine

A;Reference number: 152209; PMID:86050639; PMID:3933505

A;Accession: 152209

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 145-161 <NMG1>

A;Cross-references: GB:X03027; NID:G340174; PIDN:AAA61257.1; PID:G340175

R;Nagai, M.; Hiramatsu, K.; Kaneda, T.; Hayasue, N.; Arimura, H.; Nishida, M.; Suyama, J

Gene 36, 183-189, 1985

A;Title: Molecular cloning of cDNA coding for human preprourokinase.

A;Reference number: J0102; PMID:86056954; PMID:2415429

A;Accession: J0102

A;Molecule type: mRNA

A;Residues: 1-215; T, 215-431 <NMG2>

A;Cross-references: GB:X03226; NID:G340155; PIDN:AAC97138.1; PID:G340158; GB:D00244; NID

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 A>Title: Identification and primary sequence of an unspliced human urokinase poly(A) + RN
 A/Reference number: A37561; PMID:84272706; PMID:6589620
 A/Accession: A37561
 A/Molecule type: mRNA
 A/Residues: 66-431 <VER>
 A/Cross-references: GB:D00244; NID:9220138
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 A>Title: Molecular cloning, sequencing, and expression in Escherichia coli of human pre
 A/Reference number: I38102; PMID:85203359; PMID:3888571
 A/Accession: I38102
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-150, 'W', 152-213, 'T', 215-385, 'C', 387-429, 'V', 431 <JAC>
 A/Cross-references: EMBL:X02760; NID:935297; PIDN:CA26535.1; PID:935298
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 A/Reference number: S65783; PMID:86186279; PMID:8652631
 A/Accession: S65783
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 21-140, 'L', 142-213, 'T', 215-431 <YOS>
 A/Cross-references: EMBL:D1143; NID:9311467; PIDN:BA01919.1; PID:93119928
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 A/Accession: A37562
 A/Molecule type: protein
 A/Residues: 21-177 <GUN>
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 A/Reference number: A37563; PMID:83003608; PMID:6749491
 A/Accession: A37563
 A/Molecule type: protein
 A/Residues: 156-176, 179-193, 'T', 195, 'T', 197-224 <SCH>
 R,Steffens, G.J.; Gunzler, W.A.; Octing, F.; Frankus, E.; Flohe, L.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 1043-1058, 1982
 A>Title: The complete amino acid sequence of low molecular mass urokinase from human ur
 A/Reference number: A37564; PMID:8305099; PMID:6754572
 A/Accession: A37564
 A/Molecule type: protein
 A/Residues: 158-410 <STE>
 R,Kentzer, E.J.; Buko, A.; Menon, G.; Sarin, V.K.
 Biochem. Biophys. Res. Commun. 171, 401-406, 1990
 A>Title: Carbohydrate composition and presence of a fucose-protein linkage in recombinat
 A/Reference number: A35689; PMID:90365737; PMID:2393398
 A/Accession: A35689
 A/Molecule type: protein
 A/Residues: 21-30, 'X', 32, 'X', 34-38, 'X', 40-43 <KEN>
 A/Notes: Identification of a fucose and attempt to determine its attachment site
 R,Rabiani, S.A.; Desjardins, J.; Bell, A.W.; Benville, D.; Mazar, A.; Henkin, J.; Goltz
 Biochem. Biophys. Res. Commun. 173, 1056-1064, 1990
 A>Title: An amino-terminal fragment of urokinase isolated from a prostate cancer cell li
 A/Reference number: A36697; PMID:91097529; PMID:2125213
 A/Accession: A36697
 A/Molecule type: protein
 A/Residues: 21-34 <RAB>
 R, Li, X.; Bokman, A.M.; Linas, M.; Smith, R.A.G.; Dobson, C.M.
 submitted to the Brookhaven Protein Data Bank, July 1993
 A/Reference number: A51255; PDB:1XDU
 A/Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residu
 R, Li, X.; Smith, R.A.G.; Dobson, C.M.
 Biochemistry 31, 9562-9571, 1992
 A>Title: Sequential (1)H NMR assignments and secondary structure of the kringe domain f
 A/Reference number: A43475; PMID:33003110; PMID:1327118
 A/Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR
 R,Hansen, A.P.; Petros, A.M.; Meadows, R.P.; Nettesheim, D.G.; Mazar, A.P.; Olejniczak,
 submitted to the Brookhaven Protein Data Bank, January 1994

A/Reference number: A66822; PDB:1URK
 A/Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residues
 R, Spraggon, G.S.; Phillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobson, C.M.;
 submitted to the Brookhaven Protein Data Bank, July 1995
 A/Reference number: A66058; PDB:1LMW
 A/Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 168-175, 179-426
 C/Comment: This enzyme is found in urine in a high molecular mass form, consisting of A
 C/Comment: Urokinase-type plasminogen activator proteolytically activates plasminogen, ar
 C/Genetics: GDB:PLAU
 A/Genes: GDB:PLAU
 A/Cross-references: GDB:119497; OMIM:191840
 A/Map position: 10q24-10q24
 A/Introns: 19/3; 29/1; 65/1; 123/2; 154/1; 227/2; 277/1; 324/1; 373/3
 C/Function:
 A/Description: proteolytically activates plasminogen
 A/Pathway: Fibrinolysis
 C/Superfamily: urokinase-type plasminogen activator; EGF homology; kringe homology; try
 C/Keywords: fibrinolysis; glycoprotein; heterodimer; hydrolase; kringe; serine proteina
 F/1-20/Domains: signal sequence #status predicted <Sig>
 F/21-431/Product: urokinase-type plasminogen activator, single chain form #status predict
 F/21-177/Product: urokinase-type plasminogen activator, chain A #status experimental <MP
 F/31-62/Domains: EGF homology <EGF>
 F/70-151/Domains: kringe homology <KRG>
 F/156-177/Product: urokinase-type plasminogen activator chain A1 #status experimental <MP
 F/179-431/Product: urokinase-type plasminogen activator chain B #status experimental <MP
 F/179-419/Domains: trypsin homology <TRY>
 F/31-39,33-51,53-62,70-151,91-133,122-166,168-299,209-225,217-288,313-382,345-361,372-40
 F/38/Binding site: carbohydrate (Thr) (covalent) #status predicted
 F/178-179/Cleavage site: Lys-116 (plasmin) #status experimental
 F/224,275,376/Active site: His, Asp, Ser #status experimental
 F/322/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 44; DB 1; Length 433;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 156 KPSPPEE 163
 |||||
 |||||

RESULT 2

U-Plasminogen activator (RC 3.4.21.73) precursor - yellow baboon
 C/Species: Papio cynocephalus; Papio hamadryas cynocephalus (yellow baboon)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999
 C/Accession: S14687; S08651
 R/Au, Y.P.T.; Wang, T.W.; Clowes, A.W.
 Nucleic Acids Res. 18, 3411, 1990
 A>Title: Nucleotide and deduced amino acid sequences of baboon urokinase-type plasminoge
 A/Reference number: S14687; PMID:90287734; PMID:2113276
 A/Accession: S14687
 A/Molecule type: mRNA
 A/Residues: 1-433 <AU>
 A/Cross-references: EMBL:X51935; NID:938130; PIDN:CA36200.1; PID:938131
 C/Superfamily: urokinase-type plasminogen activator; EGF homology; kringe homology; try
 C/Keywords: glycoprotein; heterodimer; hydrolase; kringe; serine proteinase
 F/1-20/Domains: signal sequence #status predicted <Sig>
 F/21-176/Product: plasminogen activator chain A #status predicted <ACH>
 F/30-61/Domains: EGF homology <EGF>
 F/69-150/Domains: kringe homology <KRG>
 F/178-433/Product: plasminogen activator chain B #status predicted <BCH>
 F/178-421/Domains: trypsin homology <TRY>
 F/167-298,208-224,216-287,315-384,347-363,374-402/Disulfide bonds: #status predicted
 F/223,274,376/Active site: His, Asp, Ser #status predicted
 F/324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 44; DB 1; Length 433;
 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPSPPEE 8
 |||||

R:Lamerdin, J.E.; McCreedy, P.M.; Skowronski, E.; Adamson, A.W.; Burkhardt-Schultz, K.; Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; Attix, C.; Andreise, T.; Trankhel, submitted to the EMBL Data Library, March 1998
 A:Authors: Duree, S.; Lucas, S.; Bruce, R.; Thomas, P.; Quan, G.; Kronmiller, B.; Arell, A:Description: Sequence analysis of a human PI clone containing the XCC9 DNA repair gene
 A:Reference number: Z14637
 A:Accession: T02245
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-880 <LM>
 A:Cross-references: EMBL:AC004472; NID:G2984582; PID:AC07985.1; PID:G2984587
 C:Genetics:
 A:Map position: 9
 A:Introns: 89/3; 152/1; 200/1; 241/2; 294/3; 354/3; 435/1; 733/1; 802/1; 871/1

Query Match 81.8%; Score 36; DB 2; Length 880;
 Best Local Similarity 85.7%; Pred. No. 3.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PSSPPE 8
 Db 289 PSSPPE 295

RESULT 8

T46428
 hypothetical protein DKFZp434B2226.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000

C:Accession: T46428

R:Anorge, W.; Winkler, U.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23028

A:Accession: T46428

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1185 <AA>

A:Cross-references: EMBL:AL137357

A:Experimental source: adult testis; clone DKFZp434B2226

C:Genetics:
 A:Note: DKFZp434B2226.1

Query Match 81.8%; Score 36; DB 2; Length 1185;
 Best Local Similarity 85.7%; Pred. No. 4.2e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PSSPPE 8
 Db 578 PSSPPE 584

RESULT 9

A29360
 SIR4 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YD934.12; protein YDR227W; STE9 protein

C:Species: Saccharomyces cerevisiae

C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jul-2000

C:Accession: A29360; S47935; S59434; S53988; S47476; S47950

R:Marshall, M.; Mahoney, D.; Rose, A.; Hicks, J.B.; Broach, J.R.
 Mol. Cell. Biol. 7, 4441-4452, 1987

A:Title: Functional domains of SIR4, a gene required for position effect regulation in S

A:Reference number: A29360; NID:88142836; PMID:3325825

A:Accession: A29360

A:Molecule type: DNA

A:Residues: 1-1358 <MAR>

A:Cross-references: GB:M37249; NID:G531115; PID:AAA20881.1; PID:G531116

R:Davies, C.J.; Hutchison III, C.A.

submitted to the EMBL Data Library, September 1994

A:Description: Tm3 transposon/deletion sequencing of a 9.4kb DNA fragment. Characterist

A:Accession: S47935

A:Reference number: S47932

A:Residues: 1-993, 'L', '995-1358 <DAV>

A:Cross-references: EMBL:L35344; EMBL:U13239; EMBL:Z36548
 R:Murphy, L.; Harris, D.
 submitted to the EMBL Data Library, March 1995

A:Reference number: S59423

A:Accession: S59434

A:Molecule type: DNA

A:Residues: 1-1358 <MUR>

A:Cross-references: EMBL:Z48612; NID:G728671; PID:G728683; MIPS:YDR227W

R:Davies, C.J.; Hutchison III, C.A.

Nucleic Acids Res. 23, 507-514, 1995

A:Title: Insertion site specificity of the transposon Tm3.

A:Reference number: S53985; NID:95192063; PMID:7685847

A:Accession: S53988

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-993, 'L', '995-1358 <DAV>

A:Cross-references: EMBL:U13239; NID:G532747; PID:AA03144.1; PID:G532751

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994

C:Genetics:
 A:Gene: SGD:SIR4; STE9

A:Cross-references: SGD:S0002635; MIPS:YDR227W

A:Map position: 4R

C:Keywords: DNA binding; transcription regulation

Query Match 81.8%; Score 36; DB 2; Length 1358;
 Best Local Similarity 85.7%; Pred. No. 4.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPE 7
 Db 1131 KPSSPPE 1137

RESULT 10

CGHUIE

collagen alpha 1(XI) chain precursor - human

N:Alternate names: procollagen alpha 1(XI) chain

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1990 #sequence_revision 03-Oct-1995 #text_change 08-May-1998

C:Accession: A35239; A31795

R:Yoshioke, H.; Ramirez, F.

J. Biol. Chem. 265, 6423-6426, 1990

A:Title: Pro-alpha1(XI) collagen. Structure of the amino-terminal propeptide and expressi

A:Reference number: A35239; NID:90202924; PMID:1690726

A:Accession: A35239

A:Molecule type: mRNA

A:Residues: 1-558 <YOS>

A:Cross-references: GB:J05407

R:Bernard, M.; Yoshioke, H.; Rodriguez, E.; van der Rest, M.; Kimura, T.; Ninomiya, Y.; C

U. Biol. Chem. 263, 17159-17166, 1988

A:Title: Cloning and sequencing of pro-alpha1(XI) collagen cDNA demonstrates that type XI

cartilagenous tissue.

A:Reference number: A92689; NID:89034222; PMID:3182841

A:Accession: A31795

A:Molecule type: DNA; mRNA

A:Residues: 538-1806 <BER>

A:Cross-references: GB:J04177

A:Note: parts of this sequence were determined by protein sequencing

C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C

ed and subsequently O-glycosylated.

C:Genetics:
 A:Gene: GDB:COL1A1; COL16

A:Cross-references: GDB:120595; OMIM:120280

A:Map position: 1p21-1p21

A:Introns: 561/3; 579/3; 615/3; 633/3; 648/3; 666/3; 681/3

A:Note: the list of introns is incomplete

C:Complex: type XI collagen may be a heterotrimer of two alpha 1(XI) chains and one alpha

3(XI) chain (see PIR:G0H6C), initially linked by disulfide bonds among their carboxyl-ter

med with desmosome cross-links made from lysine and allysine residues

C:Function:
 A:Description: structural component of extracellular fibrous polymer associated with cell

A:Note: may play a role in controlling the lateral growth of collagen II fibrils

C:Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology
C:Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyproline
F:1-36/Domain: signal sequence #status predicted <SIG>
F:35-260/Domain: PAPP-like #status predicted <PAPP>
F:37-511/Domain: amino-terminal propeptide #status predicted <PRO>
F:512-1565/Product: collagen alpha 1(XI) chain #status predicted <ANT>
F:512-527/Region: amino-terminal nonhelical telopeptide
F:528-1542/Region: helical
F:1543-1565/Region: carboxyl-terminal nonhelical telopeptide
F:1566-1806/Domain: carboxyl-terminal propeptide #status predicted <CRP>
F:1583-1805/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
F:51-243,182-236/Disulfide bonds: #status predicted
F:505/Modified site: allylsine (Lys) #status predicted
F:512,1452/Modified site: 5-hydroxylysine (Lys) #status predicted
F:512,1452/Binding site: carboxylate (Lys) (covalent) #status predicted

Query Match 81.8%; Score 36; DB 1; Length 1806;
Best Local Similarity 75.0%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
Db 392 KPSPPEE 399

RESULT 11
B83542
hypothetical protein PA0818 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C/Accession: B83542
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitsuuchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A>Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: B83542
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <STO>
A/Cross-references: GB:AE004517; GB:AE004091; NID:9946710; PIDN:AA004207.1; GSPDB:GN001
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA0818

Query Match 79.5%; Score 35; DB 2; Length 90;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
Db 44 KPSPPEE 51

RESULT 12
T26841
hypothetical protein Y43F4B.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T26841
R:Matthews, L.
submitted to the EMBL Data Library, January 1998
A/Reference number: Z20276
A/Accession: T26841
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-216 <WTL>
A/Cross-references: EMBL:AL021481; PIDN:CAA16332.1; CESP:Y43F4B.3
A/Experimental source: clone Y43F4B
C/Genetics:
A/Gene: CESP:Y43F4B.3
A/Introns: 59/2

Query Match 79.5%; Score 35; DB 2; Length 216;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
Db 68 KPSPPEE 75

RESULT 13
H72858
apoptosis inhibitor - Autographa californica nuclear polyhedrosis virus
C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A/Note: d6DNA virus
C>Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
C/Accession: H72858
R:Atres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A>Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A/Reference number: A72850; MUID:94303173; PMID:8030224
A/Accession: H72858
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <AIR>
A/Cross-references: GB:I22858; NID:9510708; PIDN:AAA66701.1; PID:9559140
C/Genetics:
A/Gene: Ac-IAP2

Query Match 79.5%; Score 35; DB 2; Length 249;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
Db 186 KPSPPEE 193

RESULT 14
T41814
IAP2 orf71 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BMSNPV
A/Variety: isolate T3
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C/Accession: T41814
R:Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A>Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A/Reference number: Z22020; MUID:99281911; PMID:10355780
A/Accession: T41814
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-249 <RAM>
A/Cross-references: EMBL:U3180; PIDN:AA063743.1
A/Experimental source: isolate T3
C/Genetics:
A/Note: IAP2

Query Match 79.5%; Score 35; DB 2; Length 249;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
Db 186 KPSPPEE 193

RESULT 15
T07887
G box-binding protein homolog GBF1 - rape
C:Species: Brassica napus (rape)
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 26-May-2000
C/Accession: T07887

R:Bellemare, G.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: Z16192
 A:Accession: T07887
 A:Species: *Brassica napus* (rape)
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-374 <BEL>
 A:Cross-references: EMBL:U27108; NID:g1399006; PIDN:AA03379.1; PID:g1399007
 A:Experimental source: cv. Westar; roots from mature plants
 C:Genetics:
 A:Gene: GBF1
 A:Introns: 21/3
 C:Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domain homology
 C:Keywords: DNA binding; leucine zipper; transcription factor; transcription regulation
 F:253-293/Domain: fos/jun DNA-binding domain homology <F0D>

Query Match 79.5%; Score 35; DB 2; Length 374;
 Best Local Similarity 75.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 16
 T07882
 G box-binding protein homolog GBF2 - rape
 C:Species: *Brassica napus* (rape)
 C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 26-May-2000
 A:Accession: T07882
 R:Bellemare, G.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: Z16192
 A:Accession: T07882
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-376 <BEL>
 A:Cross-references: EMBL:U27107; NID:g1399004; PIDN:AA03378.1; PID:g1399005
 A:Experimental source: cv. Westar; roots from mature plants
 C:Genetics:
 A:Introns: 21/3; 36/3; 69/3; 97/3; 109/3; 175/3; 192/1; 256/3; 282/3; 324/3
 A>Note: BNGBF2
 C:Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domain homology
 C:Keywords: DNA binding; leucine zipper; transcription factor; transcription regulation
 F:253-295/Domain: fos/jun DNA-binding domain homology <F0D>

Query Match 79.5%; Score 35; DB 2; Length 376;
 Best Local Similarity 75.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
 DB 15 KPSSPAD 22

RESULT 17
 D69316
 mRNA 3'-end processing factor homolog - *Archaeoglobus fulgidus*
 C:Species: *Archaeoglobus fulgidus*
 C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
 A:Accession: D69316
 R:Plenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Uetzerack, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: D69316
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A:Residues: 1-407 <KLE>
 A:Cross-references: GB:AE001067; GB:AE000782; NID:g2689390; PIDN:AA09702.1; PID:g2650084

Query Match 79.5%; Score 35; DB 2; Length 407;
 Best Local Similarity 85.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSSPPE 7
 DB 30 KPSSDPE 36

RESULT 18
 I50213
 protein-tyrosine-phosphatase (EC 3.1.3.48) - chicken (fragment)
 C:Species: *Gallus gallus* (chicken)
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jan-2000
 A:Accession: I50213
 R:Stoker, A.W.
 Mech. Dev. 46, 201-217, 1994
 A:Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase are
 A:Reference number: I50212; MUID:95001563; PMID:7918104
 A:Accession: I50213
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-440 <STO>
 A:Cross-references: GB:I32781; NID:g485748; PIDN:AA64461.1; PID:g485749
 C:Genetics:
 A:Gene: CRYPALpha2
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; 3
 C:Keywords: phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:123-214/Domain: fibronectin type III repeat homology <F0R>

Query Match 79.5%; Score 35; DB 2; Length 440;
 Best Local Similarity 62.5%; Pred. No. 2.2e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
 DB 20 KPSPAPD 27

RESULT 19
 E96583
 hypothetical protein F20D21.4 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
 A:Accession: E96583
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: E96583
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-516 <STO>
 A:Cross-references: GB:AE005173; NID:g4585966; PIDN:AA025602.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F20D21.4
 A:Map position: 1
 C:Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology

Query Match 79.5%; Score 35; DB 2; Length 516;
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPE 7
 :|||||
 Db 203 QPSSPPE 209

RESULT 20

BABOH

peptide-aspartate beta-dioxygenase (EC 1.14.11.16) - bovine
 N:Alternate names: aspartyl (asparaginyl) beta-hydroxylase
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 31-Dec-1993 #sequence_revision 10-Feb-1995 #text_change 11-Jun-1999
 C/Accession: A42869; A39470; B39470; C39470; S27948
 R:Jia, S.; Vandusen, W.J.; Diehl, R.E.; Kohl, N.E.; Dixon, R.A.; Elliston, K.O.; Stern, J. Biol. Chem. 267, 14322-14327, 1992
 A>Title: cDNA cloning and expression of bovine aspartyl (asparaginyl) beta-hydroxylase.
 A/Reference number: A42869; PMID:2232546; PMID:11378441
 A/Accession: A42869
 A:Molecule type: mRNA
 A/Residues: 1-754 <UIA>
 A/Cross-references: EMBL:M91213; NID:G162693; PIDN:AAA03563.1; PID:G162694
 A/Experimental source: brain
 A/Note: sequence extracted from NCBI backbone (NCBI:P108534)
 R:Kang, Q.; Vandusen, W.J.; Petroski, C.J.; Garsky, V.M.; Stern, A.M.; Friedman, P.A. J. Biol. Chem. 266, 14004-14010, 1991
 A>Title: Bovine liver aspartyl beta-hydroxylase. Purification and characterization.
 A/Reference number: A39470; PMID:91310689; PMID:1856229
 A/Accession: A39470
 A:Molecule type: Protein
 A/Residues: 289-328 <MAN>
 A/Accession: B39470
 A:Molecule type: Protein
 A/Residues: 615,'X', 617-630,'XX', 633-634,'X', 636,'XX', 639-641 <WA2>
 A/Accession: C39470
 A:Molecule type: Protein
 A/Residues: 311-347,'X', 349,'X', 351-373,'X', 375-379,'X', 381-382 <WA3>
 C/Comment: This enzyme uses ferrous iron as a cofactor, and while beta-hydroxylating the C/Comment: Aspartic acid and asparagine residues in the BGF homology domain of certain P C/Superfamily: peptidic-aspartate beta-dioxygenase; tetratricopeptide repeat homology
 C/Keywords: glycoprotein; oxidoreductase; transmembrane protein
 F:2-56/Domain: intracellular #status predicted <IN>
 F:57-78/Domain: transmembrane #status predicted <TM>
 F:289-754/Product: peptidic-aspartate beta-dioxygenase, 56k form #status predicted <56k>
 F:11-754/Product: peptidic-aspartate beta-dioxygenase, 52k form #status predicted <52k>
 F:337-370/Domain: tetratricopeptide repeat homology <TT1>
 F:371-404/Domain: tetratricopeptide repeat homology <TT2>
 F:13, 96, 466, 702/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 79.5%; Score 35; DB 1; Length 754;
 Best Local Similarity 75.0%; Pred. No. 3.8e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSSPPE 8
 :|||||
 Db 134 KPVSPPPE 141

RESULT 21
 A53047
 6-phosphofructokinase (EC 2.7.1.11) - rat
 C/Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 12-May-2003
 C/Accession: A53047
 R:Cekakis, N.; Johnson, R.C.; Jenkins, A.; Maine, R.E.; Sul, H.S. J. Biol. Chem. 269, 3348-3355, 1994
 A>Title: Structure, distribution, and functional expression of the phosphofructokinase C A/Reference number: A53047; PMID:9414828; PMID:8106374
 A/Accession: A53047
 A:Molecule type: mRNA
 A/Status: preliminary
 A:Molecule type: mRNA
 A/Residues: 1-765 <GEK>
 A/Cross-references: GB:125387; NID:g466512; PIDN:AA17757.1; PID:g473914
 A/Note: authors translated the codon CCG for residue 220 as Asp

C/Superfamily: 6-phosphofructokinase, eukaryotic type: 6-phosphofructokinase 1 homology
 C/Keywords: ATP; phosphotransferase
 F:4-313/Domain: 6-phosphofructokinase 1 homology <6PF1>
 F:390-676/Domain: 6-phosphofructokinase 1 homology <6PF2>

Query Match 79.5%; Score 35; DB 2; Length 765;
 Best Local Similarity 85.7%; Pred. No. 3.9e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PSSPPE 8
 :|||||
 Db 217 PSSPPE 223

RESULT 22

JC2055

6-phosphofructokinase (EC 2.7.1.11), platelet - human
 N:Alternate names: ATP-D-fructose-6-phosphate 1-phosphotransferase
 C/Species: Homo sapiens (man)
 C>Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 12-May-2003
 C/Accession: JC2055; JH0477
 R:Ero, K.; Sakura, H.; Yasuda, K.; Hayakawa, T.; Kawasaki, E.; Moriuchi, R.; Nagataki, S Biochem. Biophys. Res. Commun. 198, 990-998, 1994
 A>Title: Cloning of a complete protein-coding sequence of human platelet-type phosphofruct A/Reference number: JC2055; PMID:94161770; PMID:8117307
 A/Accession: JC2055
 A:Molecule type: mRNA
 A/Residues: 1-784 <ETO>
 A/Cross-references: DDBJ:D25328; NID:g464186; PIDN:BA04998.1; PID:g560105
 A/Experimental source: pancreatic islet
 R:Simpson, C.J.; Fothergill-Gilmore, L.A. Biochem. Biophys. Res. Commun. 180, 197-203, 1991
 A>Title: Isolation and sequence of a cDNA encoding human platelet phosphofructokinase. A/Reference number: JH0477; PMID:92028938; PMID:1834056
 A/Accession: JH0477
 A:Molecule type: mRNA
 A/Residues: 1'P', 486-497, 499-698, 'E', 700-784 <SIM>
 A/Cross-references: GB:164784; NID:g189852; PIDN:AAA6435.1; PID:g189853
 A/Experimental source: lymphocyte, Raji cell line
 C/Comment: This enzyme catalyzes the phosphorylation of fructose 6-phosphate to fructose C/Genes:
 A/Genes: GDB:PFKP
 A/Cross-references: GDB:119480; OMIM:171840
 A/Map position: 10p15.3-10p15.2
 C/Superfamily: 6-phosphofructokinase, eukaryotic type: 6-phosphofructokinase 1 homology
 C/Keywords: allosteric regulation; ATP; duplication; glycolysis; magnesium; phosphotransf F:27-336/Domain: 6-phosphofructokinase 1 homology <6PF1>
 F:413-699/Domain: 6-phosphofructokinase 1 homology <6PF2>
 F:203,234,236,252,262,430,434,468,688/Binding site: ADP/AMP, allosteric (Thr, Ala, Trp, F:567,625/Binding site: ATP (Lys) #status predicted

Query Match 79.5%; Score 35; DB 2; Length 784;
 Best Local Similarity 85.7%; Pred. No. 4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PSSPPE 8
 :|||||
 Db 240 PSSPPE 246

RESULT 23
 A53206
 6-phosphofructokinase (EC 2.7.1.11) C - rabbit
 N:Alternate names: phosphofructo-1-kinase C
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 12-May-2003
 C/Accession: A53206; S03880
 R:Li, Y.; Valaitis, A.P.; Lathaw, S.P.; Kwiatkowska, D.; Tripathi, R.L.; Campbell, M.C., J. Biol. Chem. 269, 5781-5787, 1994
 A>Title: Structure and expression of the cDNA for the C isozyme of phosphofructo-1-kinase A/Reference number: A53206; PMID:94164929; PMID:8119919
 A/Accession: A53206
 A/Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-791 <L1A>
 A:Cross-references: GB:U001154
 R:Valaitis, A.P.; Foe, L.G.; Kwiatkowska, D.; Latehaw, S.P.; Kemp, R.G.
 Biochim. Biophys. Acta 995, 187-194, 1999
 A:Title: The sites of phosphorylation of rabbit brain phosphofructo-1-kinase by cyclic A
 A:Reference number: S03878; PMID:89194250; PMID:2539199
 A:Accession: S03880
 A:Molecule type: protein
 A:Residues: 5-17 <VAL>
 C:Superfamily: 6-phosphofructokinase, eukaryotic type; 6-phosphofructokinase 1 homology
 C:Keywords: ATP; glycolysis; phosphoprotein; phosphotransferase
 F:27-336/Domain: 6-phosphofructokinase 1 homology <6PPI>
 F:413-699/Domain: 6-phosphofructokinase 1 homology <6PFI>

Query Match 79.5%; Score 35; DB 2; Length 791;
 Best Local Similarity 85.7%; Pred. No. 4e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PSSPPE 8
 DB 240 PSSPPE 246

RESULT 24
 G75459
 DNA-directed RNA polymerase, beta subunit - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: G75459
 R:White, O.; Eilen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Venter, J.C.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; PMID:20036896; PMID:10567266
 A:Accession: G75459
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1179 <WH1>
 A:Cross-references: GB:AE001944; GB:AE000513; NID:G6458634; PIDN:AAF10490.1; PID:G645863
 A:Experimental source: strain R1
 C:Genetic8:
 A:Gene: DR0912
 A:Map position: 1
 C:Superfamily: DNA-directed RNA polymerase beta chain

Query Match 79.5%; Score 35; DB 2; Length 1179;
 Best Local Similarity 85.7%; Pred. No. 6e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSPPE 7
 DB 140 KPSPPE 146

RESULT 25
 T12737
 tail protein - Methanobacterium phage paim2
 N:Alternate names: protein 21
 C:Species: Methanobacterium phage paim2
 C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 24-Sep-1999
 C:Accession: T12737
 R:Pfeifer, P.; Wasserfallen, A.; Stettler, R.; Leisinger, T.
 submitted to the EMBL Data Library, May 1998
 A:Description: Archaeophage Paim2 complete genomic DNA.
 A:Reference number: Z17578
 A:Accession: T12737
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1186 <PFI>
 A:Cross-references: EMBL:AF065411; NID:G3249585; PID:G3249606; PIDN:AACT7060.1
 A:Experimental source: host Methanobacterium thermoautotrophicum strain Marburg

Query Match 79.5%; Score 35; DB 2; Length 1186;
 Best Local Similarity 85.7%; Pred. No. 6.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PSSPPE 8
 DB 1065 PSSPPE 1071

RESULT 26
 D3B21
 DNA-directed DNA polymerase (EC 2.7.7.7) - human herpesvirus 2 (strain 186)
 C:Species: human herpesvirus 2
 C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 27-Oct-2003
 C:Accession: A27315
 R:Tsurumi, T.; Maeno, K.; Nishiyama, Y.
 Gene 52, 129-137, 1987
 A:Title: Nucleotide sequence of the DNA polymerase gene of herpes simplex virus type 2 ar
 A:Reference number: A27315; PMID:87277385; PMID:3038677
 A:Accession: A27315
 A:Molecule type: DNA
 A:Residues: 1-1240 <TSU>
 A:Cross-references: GB:M16321; NID:G330291; PIDN:AAA5853.1; PID:G330292
 C:Superfamily: DNA polymerase
 C:Keywords: DNA binding; DNA replication; nucleotidyltransferase

Query Match 79.5%; Score 35; DB 1; Length 1240;
 Best Local Similarity 85.7%; Pred. No. 6.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PSSPPE 8
 DB 798 PSSPPE 804

RESULT 27
 D54689
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form D precursor
 N:Alternate names: MPTP delta type D
 C:Species: protein tyrosine phosphatase, receptor type delta, splice form A
 C:Accession: D54689; A54689 (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 R:Mizuno, K.; Haegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
 Mol. Cell. Biol. 13, 5513-5523, 1993
 A:Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized
 A:Reference number: A54689; PMID:93360986; PMID:8355697
 A:Accession: D54689
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1691 <MI2>
 A:Experimental source: brain
 A:Note: sequence inconsistent with nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBI:137486, NCBI:136537)
 A:Accession: A54689
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-398,799-1691 <MI2>
 A:Experimental source: brain
 A:Note: sequence inconsistent with nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBI:136522, NCBI:136524)
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; j
 OGY
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd;
 F:42-95/Domain: immunoglobulin homology <IMW3>
 F:114-196/Domain: fibronectin type III repeat homology <FN3A>
 F:1075-1691/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:1449-1671/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F:1333/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1623/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1629/Binding site: substrate phosphate (Arg) #status predicted

Query Match 79.5%; Score 35; DB 1; Length 1691;
 Best Local Similarity 62.5%; Pred. No. 8,7e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
 |||:|:|:
 Db 399 KPSAPPOD 406

RESULT 28

S46217
 protein-tyrosine-phosphatase (EC 3.1.3.48) type sigma precursor - rat
 N:Alternate names: leukocyte common antigen-related phosphatase
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 07-May-1995 #sequence revision 03-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S46217; S51174; A49104
 R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
 Biochem. J. 302, 39-47, 1994
 A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-ph
 A:Reference number: S46216; MUID:94347119; PMID:8068021
 A:Accession: S46217
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1863 <ZMA>
 A:Cross-references: EMBL:L11587
 R:Goldstein, B.J.
 submitted to the EMBL Data Library, February 1993
 A:Reference number: S51174
 A:Accession: S51174
 A:Molecule type: mRNA
 A:Residues: 1-1788, 'G', 1790-1863 <GOL>
 A:Cross-references: EMBL:L11587; NID:9205134; PID:AC37656.1; PID:9205135
 R:Yan, H.; Grossman, A.; Wang, H.; D'Eustachio, P.; Mossie, K.; Musacchio, J.M.; Silvent
 J. Biol. Chem. 268, 24880-24886, 1993
 A:Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the ner
 A:Reference number: A49104; MUID:94043351; PMID:8227050
 A:Accession: A49104
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-596, 'R', 598-603, 'I', 967-1788, 'G', 1790-1863 <YAN>
 A:Experimental source: brain
 A>Note: sequence extracted from NCBI backbone (NCBIP:139669)
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy

C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-1863/Product: protein-tyrosine-phosphatase #status predicted <MAT>
 F:149-209/Domain: immunoglobulin homology <IMM1>
 F:246-300/Domain: immunoglobulin homology <IMM2>
 F:318-400/Domain: fibronectin type III repeat homology <FN3A>
 F:413-499/Domain: fibronectin type III repeat homology <FN3B>
 F:511-592/Domain: fibronectin type III repeat homology <FN3C>
 F:1244-1863/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:1331-1552/Domain: protein-tyrosine-phosphatase homology <PRP1>
 F:1504/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1510/Binding site: substrate phosphate (Arg) #status predicted
 F:1795/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1801/Binding site: substrate phosphate (Arg) #status predicted

Query Match 79.5%; Score 35; DB 2; Length 1863;
 Best Local Similarity 62.5%; Pred. No. 9,6e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
 |||:|:|:
 Db 604 KPSAPPOD 611

RESULT 29

C54689
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor
 N:Alternate names: MPTP delta type B/C

N:Contains: protein tyrosine phosphatase, receptor type delta, splice form C
 C:Species: Mus musculus (house mouse)
 C>Date: 25-Apr-1995 #sequence revision 19-May-1995 #text_change 12-Feb-1999
 C:Accession: C54689; B54689
 R:Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
 Mol. Cell. Biol. 13, 5513-5523, 1993
 A:Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized
 A:Reference number: A54689; MUID:93360986; PMID:8355697
 A:Accession: C54689
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1894 <MIZ>
 A:Experimental source: brain; splice form B
 A>Note: sequence inconsistent with nucleotide translation
 A>Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIP:137487)
 A:Accession: B54689
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-352, 'H', 354-535, 'S', 537-601, 1002-1894 <MIZ>
 A:Experimental source: brain; splice form C
 A>Note: sequence inconsistent with nucleotide translation
 A>Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIP:136530)
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy

C:Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hyd
 F:45-107/Domain: immunoglobulin homology <IMM1>
 F:245-299/Domain: immunoglobulin homology <IMM2>
 F:317-399/Domain: fibronectin type III repeat homology <FN3A>
 F:1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:1652-1874/Domain: protein-tyrosine-phosphatase homology <PRP2>
 F:1536/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1542/Binding site: substrate phosphate (Arg) #status predicted
 F:1826/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1832/Binding site: substrate phosphate (Arg) #status predicted

Query Match 79.5%; Score 35; DB 2; Length 1894;
 Best Local Similarity 62.5%; Pred. No. 9,7e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
 |||:|:|:
 Db 602 KPSAPPOD 609

RESULT 30

S50893
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 01-Aug-1995 #sequence revision 01-Sep-1995 #text_change 21-Jan-2000
 C:Accession: S50893; S40281
 R:Wagner, J.; Boerboom, D.; Tremblay, M.L.
 Eur. J. Biochem. 226, 773-782, 1994
 A:Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type I
 A:Reference number: S50893; MUID:95112841; PMID:7529177
 A:Accession: S50893
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1907 <WAG>
 A:Cross-references: EMBL:X82288; NID:9587483; PID:CAA57732.1; PID:9587484
 R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
 submitted to the EMBL Data Library, June 1993
 A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
 A:Reference number: S40280
 A:Accession: S40281
 A:Molecule type: mRNA
 A:Residues: 1441-1501, 'E', 1503-1546 <HEN>
 A:Cross-references: EMBL:Z23050; NID:9438137; PID:CAA80585.1; PID:9438138
 C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 ogy

C:Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane p
 F:149-209/Domain: immunoglobulin homology <IMM1>
 F:246-300/Domain: immunoglobulin homology <IMM2>
 F:413-506/Domain: fibronectin type III repeat homology <FN3A>

F:1288-1907/Domain: leukocyte common antigen cytosolic domain homology <LAC>
 F:1375-1596/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:1664-1687/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F:1546/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1554/Binding site: substrate phosphate (Arg) #status predicted
 F:1839/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:1845/Binding site: substrate phosphate (Arg) #status predicted

Query Match 79.5%; Score 35; DB 2; Length 1907;
 Best Local Similarity 62.5%; Pred. No. 9.8e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
 DB 604 KPSAPPD 611

RESULT 31

A56178

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human
 N/Alternate names: protein-tyrosine-phosphatase BPT-2

C/Species: Homo sapiens (man)

C/Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text_change 21-Jan-2000

C/Accession: A56178; S12052; B44929

R/Pulido, R.; Krueger, N.X.; Serra-Pages, C.; Saito, H.; Streuli, M.

J. Biol. Chem. 270, 6722-6728, 1995

A/Title: Molecular characterization of the human transmembrane protein-tyrosine phosphatase delta isoforms.

A/Reference number: A56178; UID:95204468; PMID:7896816

A/Accession: A56178

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1912 <PU>

A/Cross-references: GB:138929; NID:9755652; PIDN:AA041749.1; PID:9755653

R/Krueger, N.X.; Streuli, M.; Saito, H.

EMBO J. 9, 3241-3252, 1990

A/Title: Structural diversity and evolution of human receptor-like protein tyrosine phosphatases

A/Reference number: S12049; UID:91006018; PMID:2170109

A/Accession: S12052

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 390-1912 <RU>

A/Cross-references: GB:X54133; NID:935789; PIDN:CA38068.1; PID:935790

A/Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-T

R/Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinda, K.; Yac

Cancer Res. 52, 737-740, 1992

A/Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.

A/Reference number: A44929; UID:92119637; PMID:1370651

A/Accession: B44929

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1756-1804, 'C', 1806-1845 <AD>

A/Cross-references: GB:S78086; NID:9243545; PIDN:AA21147.1; PID:9243546

A/Experimental source: pre-B cell NALM-6

A/Note: sequence extracted from NCBI backbone (NCBI:78086, NCBI:P:78087)

A/Note: the authors did not report the entire codon for residue 90

C/Genetics: GDB:PTPRD

A/Genes: GDB:131384; OMIM:601598

A/Map position: 9p24-9p24

C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;

QY

C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane

F:138-100/Domain: immunoglobulin homology <IMM1>

F:140-209/Domain: immunoglobulin homology <IMM2>

F:150-304/Domain: immunoglobulin homology <IMM3>

F:111-811/Domain: fibronectin type III repeat homology <3PR>

F:1293-1912/Domain: leukocyte common antigen cytosolic domain homology <LAC>

F:1659-1892/Domain: protein-tyrosine-phosphatase homology <PTP2>

F:1553/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1553/Binding site: substrate phosphate (Arg) #status predicted

F:1844/Active site: Cys (phosphocysteine intermediate) #status predicted

F:1850/Binding site: substrate phosphate (Arg) #status predicted

Query Match 79.5%; Score 35; DB 2; Length 1912;
 Best Local Similarity 62.5%; Pred. No. 9.8e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8
 DB 608 KPSAPPD 615

RESULT 32

FNB0

fibronectin - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 20-Oct-2000

C/Accession: A26452; B21165; A23292

R/Skorstenggaard, K.; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S.

Eur. J. Biochem. 161, 441-453, 1986

A/Title: Complete primary structure of bovine plasma fibronectin.

A/Reference number: A26452; UID:87054047; PMID:3780752

A/Accession: A26452

A/Molecule type: protein

A/Residues: 1-2265 <SK>

R/Kornblith, A.R.; Vide-Pedersen, K.; Baralle, F.E.

Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983

A/Title: Isolation and characterization of cDNA clones for human and bovine fibronectins.

A/Reference number: A21165; UID:83221567; PMID:6304699

A/Accession: B21165

A/Molecule type: mRNA

A/Residues: 2170-2265 <KOR>

A/Cross-references: GB:X00800; NID:9163055; PIDN:AA30521.2; PID:95713323

R/Petersen, T.E.; Thøgersen, H.C.; Skorstenggaard, K.; Vide-Pedersen, K.; Sahl, P.; Sotter

Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 1983

A/Title: Partial primary structure of bovine plasma fibronectin: three types of internal

A/Reference number: A23292; UID:83117805; PMID:6218503

A/Accession: A23292

A/Molecule type: protein

A/Residues: 1-16, 'C', 18-20, 'S', 22-43; 447-463; 1367-1517; 1567-1673; 2062-2176, 'N', 2178-2265

C/Comment: Cys-1201 and Cys-2015 have free sulfhydryl groups.

C/Comment: The plasma fibronectin molecule consists of two chains, which are connected by

C/Comment: Fibronectin bind cell surfaces and various compounds including collagen, fibr

C/Comment: and maintenance of cell shape.

C/Comment: Plasma fibronectin is synthesized by hepatocytes.

C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe

C/Keywords: acute phase; alternative splicing; collagen binding; duplication; extracellular

F:21-241/Domain: fibronectin type I repeat homology <1P1>

F:21-241/Domain: fibronectin type I repeat homology <1P2>

F:21-241/Domain: fibronectin type I repeat homology <1P3>

F:110-148/Domain: fibronectin type I repeat homology <1P4>

F:155-194/Domain: fibronectin type I repeat homology <1P5>

F:200-239/Domain: fibronectin type I repeat homology <1P6>

F:277-577/Domain: fibronectin type I repeat homology <1P7>

F:277-577/Domain: fibronectin type I repeat homology <1P8>

F:329-370/Domain: fibronectin type II repeat homology <2P1>

F:389-430/Domain: fibronectin type II repeat homology <2P2>

F:439-477/Domain: fibronectin type I repeat homology <1P9>

F:487-524/Domain: fibronectin type I repeat homology <1P10>

F:530-568/Domain: fibronectin type I repeat homology <1P11>

F:578-661/Domain: fibronectin type III repeat homology <FN3A>

F:688-770/Domain: fibronectin type III repeat homology <FN3B>

F:779-860/Domain: fibronectin type III repeat homology <FN3C>

F:875-957/Domain: fibronectin type III repeat homology <FN3D>

F:965-1046/Domain: fibronectin type III repeat homology <FN3E>

F:1055-1134/Domain: fibronectin type III repeat homology <FN3F>

F:1142-1227/Domain: fibronectin type III repeat homology <FN3G>

F:1235-1318/Domain: fibronectin type III repeat homology <FN3H>

F:1326-1404/Domain: fibronectin type III repeat homology <FN3I>

F:1410-1517/Domain: fibronectin type III repeat homology <FN3J>

F:1416-1502/Domain: fibronectin type III repeat homology <FN3K>

F:1493-1495/Region: cell attachment (R-G-D) motif

F:1510-1592/Domain: fibronectin type III repeat homology <FN3L>

F:1600-1870/Domain: heparin binding <HB2>

F:1600-1682/Domain: fibronectin type III repeat homology <FN3M>

F:1692-1773/Domain: fibronectin type III repeat homology <FN3N>

F:1181-1863/Domain: fibronectin type III repeat homology <FN3N>
 F:1970-1972/Region: cell attachment (R-G-D) motif
 F:1982-2062/Domain: fibronectin type III repeat homology <FN3O>
 F:1985-2221/Domain: fibrin binding <FB2>
 F:2085-2124/Domain: fibronectin type I repeat homology <FI10>
 F:2110-2167/Domain: fibronectin type I repeat homology <FI1>
 F:2174-2209/Domain: fibronectin type I repeat homology <FI12>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:3/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of fibrin) #status expiring
 F:21-47,45-56,66-94,92-104,110-138,136-148,155-184,182-194,200-229,227-239,277-304,302-3
 7,2155-2167,2174-2200,2198-2209/Disulfide bonds: #status predicted
 F:399,497,511,846,976,1213,1987/Binding site: carboxylate (Asn) (covalent) #status exp
 F:1205,1692/Binding site: carboxylate (Asn) (covalent) #status absent
 F:1943,1944/Binding site: carboxylate (Thr) (covalent) #status experimental
 F:2246/Disulfide bonds: interchain (to 2250) #status predicted
 F:2250/Disulfide bonds: interchain (to 2246) #status predicted
 F:2263/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 79.5%; Score 35; DB 1; Length 2265;
 Best Local Similarity 75.0%; Pred. No. 1.2e+03;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPGSPPE 8
 Db 1818 KPGSPPE 1825

RESULT 33

FNHU
 fibronectin precursor [validated] - human
 N:Alternate names: fibronectin splice form ED-A
 C:Species: Homo sapiens (man)
 C:Date: 27-Nov-1985 #sequence, revision 31-Mar-1993 #text, change 08-Dec-2000
 C:Accession: A26460; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A22
 R:Dean, D.C.; Bowler, C.L.; Bourgeois, S.
 Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987
 A:Title: Cloning and analysis of the promoter region of the human fibronectin gene.
 A:Reference number: A26460; PMID:8715578; PMID:3031656
 A:Accession: A26460
 A:Molecule type: DNA
 A:Residues: 1-49 <DRA>
 A:Cross-references: GB:M15801; NID:g182686; PIDN:AAA53376.1; PID:g553293
 R:Oldberg, A.; Ruoslahti, E.
 J. Biol. Chem. 261, 2113-2116, 1986
 A:Title: Evolution of the fibronectin gene.
 A:Reference number: A26284; PMID:86111901; PMID:3003095
 A:Accession: A26284
 A:Molecule type: DNA
 A:Residues: 1447-1540 <OLD>
 A:Cross-references: GB:M12549; NID:g182688
 A:Note: the authors translated the codon TTC for residue 1494 as Glu
 R:Paolella, G.; Hencicliffe, C.; Sebastio, G.; Baralle, F.E.
 Nucleic Acids Res. 16, 3545-3557, 1988
 A:Title: Sequence analysis and in vivo expression show that alternative splicing of ED-E
 A:Reference number: S00848; PMID:88233940; PMID:3375063
 A:Accession: S03917
 A:Molecule type: DNA
 A:Residues: 1594-1767, 'V', 1769-1783 <PAO>
 A:Cross-references: EMBL:X07718; NID:g31402
 A:Note: the authors translated the codon AAC for residue 1631 as Asp
 R:Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.
 FEBS Lett. 207, 287-291, 1986
 A:Title: Donor and acceptor splice signals within an exon of the human fibronectin gene:
 A:Reference number: A24854; PMID:87030929; PMID:3770201
 A:Accession: A24854
 A:Molecule type: DNA
 A:Residues: 1992-2147 <VIB>
 A:Cross-references: GB:X04530; NID:g31436
 R:Gutman, A.; Yamada, K.M.; Kornblith, A.
 FEBS Lett. 207, 145-148, 1986
 A:Title: Human fibronectin is synthesized as a pre-propolypeptide.
 A:Reference number: A24476; PMID:87030890; PMID:3770189
 A:Accession: A24476

A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-14, 'Q', 16-38 <GUT>
 R:Kornblith, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.
 EMBO J. 4, 1755-1759, 1985
 A:Title: Primary structure of human fibronectin: differential splicing may generate at le
 A:Reference number: A91008; PMID:85284965; PMID:25923939
 A:Accession: A91008
 A:Molecule type: mRNA
 A:Residues: 32-144, 1346-2080; 2112-2386 <KOR>
 A:Cross-references: GB:X02761
 R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
 Nucleic Acids Res. 12, 5851-5868, 1984
 A:Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptide
 A:Reference number: A93529; PMID:84272258; PMID:6462919
 A:Accession: A93529
 A:Molecule type: mRNA
 A:Residues: 973-2080; 2112-2386 <KO2>
 A:Cross-references: GB:X00739
 R:Oldberg, A.; Linney, E.; Ruoslahti, E.
 J. Biol. Chem. 258, 10193-10196, 1983
 A:Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell at
 A:Reference number: A21011; PMID:83250929; PMID:6688418
 A:Accession: A21011
 A:Molecule type: mRNA
 A:Residues: 1434-1537 <OL2>
 A:Cross-references: GB:K00055; NID:g182680; PIDN:AAA52459.1; PID:g182683
 R:Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.
 Biochemistry 24, 2698-2704, 1985
 A:Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with rat
 A:Reference number: A90495; PMID:85280409; PMID:2992573
 A:Accession: A90495
 A:Molecule type: mRNA
 A:Residues: 1594-2386 <BER>
 A:Cross-references: GB:M10905; NID:g182696; PIDN:AAA52462.1; PID:g182697
 R:Umezawa, K.; Kornblith, A.R.; Baralle, F.E.
 FEBS Lett. 186, 31-34, 1985
 A:Title: Isolation and characterization of cDNA clones for human liver fibronectin.
 A:Reference number: A22245; PMID:85231203; PMID:2989004
 A:Accession: A22245
 A:Molecule type: mRNA
 A:Residues: 1948-2067 <UMB>
 A:Cross-references: GB:M27589; NID:g182705; PIDN:AAA52465.1; PID:g182706
 A:Accession: B22245
 A:Molecule type: mRNA
 A:Residues: 1975-1991; 2017-2039 <UM2>
 A:Cross-references: GB:M27590
 R:Seikuchi, K.; Kios, A.M.; Kiyachi, K.; Yoshitake, S.; Hakomori, S.
 Biochemistry 25, 4936-4941, 1986
 A:Title: Human liver fibronectin complementary DNAs: identification of two different mes
 A:Reference number: 152394; PMID:87026578; PMID:3021206
 A:Accession: 152394
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1978-1990, 2016-2018, 'N', 2020-2081, 2113-2127 <SEK>
 A:Cross-references: GB:M14060; NID:g182701; PIDN:AAA52464.1; PID:g182704
 R:Kornblith, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
 Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
 A:Title: Isolation and characterization of cDNA clones for human and bovine fibronectins
 A:Reference number: A21165; PMID:83221567; PMID:6504699
 A:Accession: A21165
 A:Molecule type: mRNA
 A:Residues: 2291-2386 <KO3>
 A:Cross-references: GB:K00799; NID:g182681; PIDN:AAA52460.1; PID:g182684
 R:Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
 J. Biol. Chem. 258, 12670-12674, 1983
 A:Title: Primary structure of human plasma fibronectin.
 A:Reference number: A92398; PMID:84032463; PMID:6630202
 A:Accession: A92398
 A:Molecule type: protein
 A:Residues: 32-47, 'C', 49-51, 'S', 53-72, 'A', 74-290 <GAR>
 R:Garcia-Pardo, A.; Gold, L.I.

Arch. Biochem. Biophys. 304, 181-188, 1993
 A>Title: Further characterization of the binding of fibronectin to gelatin reveals the
 A:Reference number: S34791; PMID:93312001; PMID:8323285
 A:Accession: S34791
 A:Molecule type: protein
 A:Residues: 291-300;551-560 <GAR2>
 R:Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
 Thromb. Res. 43, 469-477, 1986
 A>Title: Two plasma fibronectin fragments with different gelatin-binding properties.
 A:Reference number: A60904; PMID:87019725; PMID:3532418
 A:Accession: A60904
 A:Molecule type: protein
 A:Residues: 293-301 <GRI>
 R:Calaycay, J.; Pandey, H.; Lee, T.; Borsi, L.; Sirt, A.; Shively, J.E.; Zardi, L.
 J. Biol. Chem. 260, 12136-12141, 1985
 A>Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human p
 A:Accession: A23901; PMID:86008277; PMID:3900070
 A:Reference number: A23901
 A:Molecule type: protein
 A:Residues: 616-677 'Q', 679-703 'PT' <CAL>
 R:Pierzbacher, M.D.; Ruoslahti, E.; Sundelin, J.; Lind, P.; Peterson, P.A.
 J. Biol. Chem. 257, 9593-9597, 1982
 A>Title: The cell attachment domain of fibronectin. Determination of the primary structu
 A:Reference number: A92386; PMID:82265604; PMID:7050098
 A:Accession: A92386
 A:Molecule type: protein
 A:Residues: 1441-1548 <PIE>
 A>Note: residues 1524-1527 are responsible for the cell-binding activity
 R:Garcia-Pardo, A.; Roostagno, A.; Frangione, B.
 Biochem. J. 241, 923-928, 1987
 A>Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa dom
 A:Reference number: A32517; PMID:87241275; PMID:3593220
 A:Accession: A32517
 A:Molecule type: protein
 A:Residues: 1589-1630 'T', 1722-2058 <GAR3>
 R:Tresselt, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pand
 Biochem. J. 274, 731-738, 1991
 A>Title: Human plasma fibronectin. Demonstration of structural differences between the A
 A:Reference number: S14357; PMID:91190085; PMID:2012601
 A:Accession: S14357
 A:Molecule type: protein
 A:Residues: 1614-1630 'T', 1722-2081, 2113-2244 <TR3>
 R:Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
 J. Biol. Chem. 260, 10320-10325, 1985
 A>Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-da
 A:Reference number: A23891; PMID:85261459; PMID:4019516
 A:Accession: A23891
 A:Molecule type: protein
 A:Residues: 2071-2080; 2112-2356 <GAR4>
 C:Comment: The extra domain and connecting strand 3 are subject to developmental and tis
 C:Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins,
 ation, and transformation.
 C:Genetic:
 A:Gene: GDB:FN1
 A:Cross-references: GDB:119135; OMIM:135600
 A:Map position: 2q34-2q34
 A:Introns: 49/3; 1266//1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
 C:Superfamily: fibronectin; fibronectin type I repeat homology <1F1>
 C:Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplicat
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:27-31/Domain: propeptide #status predicted <PRO>
 F:32-2386/Product: fibronectin #status experimental <MAT>
 F:52-272/Domain: fibrin and heparin binding <FRB>
 F:52-97/Domain: fibronectin type I repeat homology <1F1>
 F:97-135/Domain: fibronectin type I repeat homology <1F2>
 F:141-179/Domain: fibronectin type I repeat homology <1F3>
 F:186-225/Domain: fibronectin type I repeat homology <1F4>
 F:231-270/Domain: fibronectin type I repeat homology <1F5>
 F:308-608/Domain: collagen binding <CBR>
 F:308-342/Domain: fibronectin type I repeat homology <1F5>
 F:360-401/Domain: fibronectin type II repeat homology <2F1>
 F:420-461/Domain: fibronectin type II repeat homology <2F2>
 F:470-508/Domain: fibronectin type I repeat homology <1F7>

F:518-555/Domain: fibronectin type I repeat homology <1F8>
 F:561-599/Domain: fibronectin type I repeat homology <1F9>
 F:609-692/Domain: fibronectin type III repeat homology <3FA>
 F:616-706/Domain: heparin binding <HBB>
 F:719-801/Domain: fibronectin type III repeat homology <3FB>
 F:810-891/Domain: fibronectin type III repeat homology <3FC>
 F:906-988/Domain: fibronectin type III repeat homology <3FD>
 F:996-1077/Domain: fibronectin type III repeat homology <3FE>
 F:1086-1164/Domain: fibronectin type III repeat homology <3FF>
 F:1173-1258/Domain: fibronectin type III repeat homology <3FG>
 F:1266-1349/Domain: fibronectin type III repeat homology <3FH>
 Query Match 79.5%; Score 35; DB 1; Length 2386;
 Best local Similarity 75.0%; Pred. No. 12e+03;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KPSPPPE 8
 Db 1939 KPSPPPE 1946
 RESULT 34
 S14428
 fibronectin precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 28-Oct-1994 #sequence revision 28-Oct-1994 #text change 20-Aug-1999
 C:Accession: S14428; S12455; A22319; S46203; S00459; A27252; I59049
 R:Hynes, R.O.
 Submitted to the EMBL Data Library, July 1989
 A:Reference number: S14428
 A:Accession: S14428
 A:Molecule type: mRNA
 A:Residues: 1-2477 <HNY>
 A:Cross-references: EMBL:X15906; NID:956163; PID:CA34020.1; PID:956164
 R:Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.
 EMBL J. 6, 2573-2580, 1987
 A>Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.
 A:Reference number: S12455; PMID:88054951; PMID:2445560
 A:Accession: S12455
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 609-1810 'T', 1812-2283 <SCH>
 A:Cross-references: EMBL:X15906
 R:Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
 A>Title: A single rat fibronectin gene generates three different mRNAs by alternative sp
 A:Reference number: A22319; PMID:84298097; PMID:6089177
 A:Accession: A22319
 A:Molecule type: DNA
 A:Residues: 2052-2237 <TAM>
 R:Palckenberg, C.; Engchild, J.J.; Thogersen, I.B.; Salvesen, G.; Akerstrom, B.
 Biochem. J. 301, 745-751, 1994
 A>Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex in
 A:Reference number: S46203; PMID:94330948; PMID:7519849
 A:Accession: S46203
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1183-1192; GLN, 1268, 'P', 1270-1271, 'D', 1273, 'CF', 1276, 'PY', 1385-1399 <PAL>
 R:Patel, R.S.; Odeh, E.; Schwarzbauer, J.E.; Hynes, R.O.
 EMBL J. 6, 2565-2572, 1987
 A>Title: Organization of the fibronectin gene provides evidence for exon shuffling during
 A:Reference number: S00459; PMID:88054950; PMID:3119923
 A:Accession: S00459
 A:Molecule type: DNA
 A:Residues: 1-139; 2382-2477 <PAT>
 A:Cross-references: EMBL:X05831
 A>Note: the authors translated the codon CCG for residues 51 and 94 as Ala
 R:Schwarzbauer, J.E.; Tamkun, J.W.; Lemischka, I.R.; Hynes, R.O.
 Cell 35, 421-431, 1983
 A>Title: Three different fibronectin mRNAs arise by alternative splicing within the codi
 A:Reference number: A27252; PMID:84082067; PMID:6317187
 A:Accession: A27252
 A:Molecule type: mRNA

A/Residues: 1586-1720,'T','1722,1813-2477 <SC2>
 P/Odermat, E.; Tamkun, J.W.; Hynes, R.O.
 Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
 A/Title: Repeating modular structure of the fibronectin gene: Relationship to protein st
 A/Reference number: 159049; MUID:66016741; PMID:3863113
 A/Accession: 159049
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1722-1810 <RES>
 A/Cross-references: GB:M11750; NID:g204164; PIDN:AAA1170.1; PID:g554437
 C/Genetics:
 A/Introns: 51/1; 94/1; 2416/3; 2454/3
 C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
 C/Keywords: alternative splicing; cell adhesion; collagen binding; disulfide bond; dupli
 F/1-32/Domain: signal sequence #status predicted <SIG>
 F/33-2477/Product: fibronectin #status predicted <MAT>
 F/53-88/Domain: fibronectin type I repeat homology <1F1>
 F/98-136/Domain: fibronectin type I repeat homology <1F2>
 F/142-180/Domain: fibronectin type I repeat homology <1F3>
 F/187-226/Domain: fibronectin type I repeat homology <1F4>
 F/232-271/Domain: fibronectin type I repeat homology <1F5>
 F/308-342/Domain: fibronectin type I repeat homology <1F6>
 F/360-401/Domain: fibronectin type II repeat homology <2F1>
 F/420-461/Domain: fibronectin type II repeat homology <2F2>
 F/470-508/Domain: fibronectin type I repeat homology <1F7>
 F/518-555/Domain: fibronectin type I repeat homology <1F8>
 F/561-599/Domain: fibronectin type I repeat homology <1F9>
 F/609-692/Domain: fibronectin type III repeat homology <FN3A>
 F/718-800/Domain: fibronectin type III repeat homology <FN3B>
 F/809-890/Domain: fibronectin type III repeat homology <FN3C>
 F/905-987/Domain: fibronectin type III repeat homology <FN3D>
 F/995-1076/Domain: fibronectin type III repeat homology <FN3E>
 F/1085-1164/Domain: fibronectin type III repeat homology <FN3F>
 F/1172-1257/Domain: fibronectin type III repeat homology <FN3G>
 F/1265-1348/Domain: fibronectin type III repeat homology <FN3H>
 F/1356-1439/Domain: fibronectin type III repeat homology <FN3I>
 F/1447-1529/Domain: fibronectin type III repeat homology <FN3J>
 F/1537-1619/Domain: fibronectin type III repeat homology <FN3K>
 F/1614-1616/Region: cell attachment (R-G-D) motif
 F/1631-1713/Domain: fibronectin type III repeat homology <FN3L>
 F/1721-1803/Domain: fibronectin type III repeat homology <FN3M>
 F/1811-1893/Domain: fibronectin type III repeat homology <FN3N>
 F/1903-1984/Domain: fibronectin type III repeat homology <FN3O>
 F/1992-2074/Domain: fibronectin type III repeat homology <FN3P>
 F/2181-2193/Region: cell attachment (R-G-D) motif
 F/2193-2273/Domain: fibronectin type III repeat homology <FN3Q>
 F/2296-2335/Domain: fibronectin type I repeat homology <1F10>
 F/2341-2378/Domain: fibronectin type I repeat homology <1F11>
 F/2385-2420/Domain: fibronectin type I repeat homology <1F12>
 F/53-79,77-88,98-126,124-136,142-170,168-180,187-216,214-226,232-261,259-271,308-335,333
 F/2458/Disulfide bonds: interchain (to 2462) #status predicted
 F/2462/Disulfide bonds: interchain (to 2458) #status predicted

Query Match 79.5%; Score 35; DB 2; Length 2477;
 Best Local Similarity 75.0%; Pred. No. 1.3e+03;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
 Db 2029 KPSPPEE 2036

RESULT 35
 AG2522
 hypothetical protein asl7359 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120a1
 C/Species: Nostoc sp. PCC 7120
 A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C/Accession: AG2522
 R/Kaneho, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anai
 A/Reference number: AB1807; MUID:21595285; PMID:11759840
 A/Accession: AG2522
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-66 <KUR>
 A/Cross-references: GB:BA000020; PIDN:BA077117.1; PID:gl7134558; GSPDB:GN00180
 A/Experimental source: strain PCC 7120
 C/Genetics:
 A/Gene: asl7359
 A/Genome: plasmid

Query Match 77.3%; Score 34; DB 2; Length 66;
 Best Local Similarity 62.5%; Pred. No. 47;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
 Db 30 KPSPPEE 37

RESULT 36
 F83167
 hypothetical protein PA3833 [imported] - Pseudomonas aeruginosa (strain PA01)
 C/Species: Pseudomonas aeruginosa
 C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C/Accession: F83167
 R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bri
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 .; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
 A/Reference number: AB2950; MUID:20437337; PMID:10984043
 A/Accession: F83167
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-122 <STO>
 A/Cross-references: GB:AE004800; GB:AE004091; NID:g9949999; PIDN:AA07220.1; GSPDB:GN001;
 A/Experimental source: strain PA01
 C/Genetics:
 A/Gene: PA3833

Query Match 77.3%; Score 34; DB 2; Length 122;
 Best Local Similarity 62.5%; Pred. No. 88;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPSPPEE 8
 Db 5 KPSPPEE 12

RESULT 37
 H82468
 hypothetical protein VCA0370 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C/Species: Vibrio cholerae
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C/Accession: H82468
 R/Heldberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bas, S.; Qin, H.; Dragoi, I.; Sellers, P
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A/Reference number: AB2035; MUID:20406833; PMID:10952301
 A/Accession: H82468
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-124 <HET>
 A/Cross-references: GB:AE004373; GB:AE003853; NID:g9657758; PIDN:AAF6277.1; GSPDB:GN001;
 A/Experimental source: serogroup O1; strain N16961; biotype El Tor
 C/Genetics:
 A/Gene: VCA0370; VCA0369
 A/Map position: 2

Query Match 77.3%; Score 34; DB 2; Length 124;
 Best Local Similarity 85.7%; Pred. No. 90;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSSPP 7
 |||||
 DB 62 KPSSPPE 68

RESULT 38

E72759
 Hypothetical protein APE0066 - Aeropyrum pernix (strain K1)

C/Species: Aeropyrum pernix
 C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000

C/Accession: E72759
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999

A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
 A/Reference number: A72450; PMID:99310339; PMID:10382966

A/Accession: E72759

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-136 <RAM>

A/Cross-references: DDBJ:AP000058; NID:G5103388; PIDN:BAA78975.1; PID:dl042751; PID:G5103388

A/Experimental source: strain K1

C/Genetics:

A/Gene: APE0066

C/Superfamily: Aeropyrum pernix hypothetical protein APE0066

Query Match 77.3%; Score 34; DB 2; Length 136;
 Best Local Similarity 75.0%; Pred. No. 98;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSSPPE 8
 |||||
 DB 35 KPSSPPE 42

RESULT 39

E72505
 Hypothetical protein APE2019 - Aeropyrum pernix (strain K1)

C/Species: Aeropyrum pernix
 C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000

C/Accession: E72505

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999

A/Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
 A/Reference number: A72450; PMID:99310339; PMID:10382966

A/Accession: E72505

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-140 <RAM>

A/Cross-references: DDBJ:AP000063; NID:G5105654; PIDN:BAA81029.1; PID:dl044815; PID:G5105654

A/Experimental source: strain K1

C/Genetics:

A/Gene: APE2019

C/Superfamily: Aeropyrum pernix hypothetical protein APE2019

Query Match 77.3%; Score 34; DB 2; Length 140;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPP 6
 |||||
 DB 86 KPSSPP 91

RESULT 40

T31243
 Hypothetical protein 915 - Sphingomonas aromaticivorans plasmid pNL1

C/Species: Sphingomonas aromaticivorans

C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jun-2000

C/Accession: T31243

R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thureston, S.J.; Sisk, E.C.; Sensen, C.W.; Ge submitted to the EMBL Data Library, July 1998

A/Description: Complete sequence of a 184 kb catapolic plasmid from Sphingomonas aromaticivorans

A/Reference number: Z20992

A/Accession: T31243

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-173 <ROM>

A/Cross-references: EMBL:AF079317; NID:G3378261; PID:G3378383; PIDN:AAD03966.1

C/Genetics:

A/Genome: plasmid pNL1

A/Note: orf915

C/Superfamily: Sphingomonas aromaticivorans hypothetical protein 915

Query Match 77.3%; Score 34; DB 2; Length 173;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPP 6
 |||||
 DB 13 KPSSPP 18

RESULT 41

H82155
 Hypothetical protein VCI1788 VCA0370 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C/Species: Vibrio cholerae

C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C/Accession: H82155; A82469

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chaudson, D.; Ermocheva, M.D.; Venter, J.C.; Fraser, C.M.

1, R.R.; Mekalanos, M.D.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A/Title: DNA Sequence of Both chromosomes of the cholera pathogen Vibrio cholerae.

A/Reference number: A82035; PMID:10406833; PMID:10952301

A/Accession: H82155

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-231 <H81>

A/Cross-references: GB:AE004256; GB:AE003852; NID:G9656310; PIDN:AAF94937.1; GSPDB:GN0012

A/Experimental source: serogroup O1; strain N16961; biotype El Tor

A/Accession: A82469

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-231 <H82>

A/Cross-references: GB:AE004373; GB:AE003853; NID:G9657758; PIDN:AAF96276.1; GSPDB:GN0012

A/Experimental source: serogroup O1; strain N16961; biotype El Tor

C/Genetics: <GEN1>

A/Gene: VCI1788

A/Map position: 1

C/Genetics: <GEN2>

A/Genes: VCA0370

A/Map position: 2

Query Match 77.3%; Score 34; DB 2; Length 231;
 Best Local Similarity 85.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KPSSPPE 7
 |||||
 DB 169 KPSSPPE 175

RESULT 42

A60548
 synaptohyrin - Pacific electric ray

C/Species: Torpedo californica (Pacific electric ray)

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 04-Sep-1998

C/Accession: A60548

R:Cowan, D.; Linial, M.; Scheller, R.H.

Brain Res. 509, 1-7, 1990

A>Title: Torpedo synaptophysin: evolution of a synaptic vesicle protein.
A/Reference number: A60548; MUID:90167450; PMID:2106365
A/Accession: A60548
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-301 <COM>
C/Superfamily: synaptophysin
C/Keywords: channel-forming protein; glycoprotein; hexamer; membrane protein; phosphoric

Query Match 77.3%; Score 34; DB 2; Length 301;
Best Local Similarity 75.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
Db 229 KPGLPPEE 236

RESULT 43

TJ33972
hypothetical protein DC2.3 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C/Accession: TJ33972
R/Bauer, C.; Sammons, L.; Wohlman, P.; Chiapelli, B.
submitted to the EMBL Data Library, February 1999
A/Description: The sequence of C. elegans cosmid DC2.
A/Reference number: Z21447

A/Accession: TJ33972
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-310 <BNV>
A/Cross-references: EMBL:AF125956; PIDN:AA14724.1; GSPDB:GN00023; CESP:DC2.3
A/Experimental source: strain Bristol N2; clone DC2
C/Genetics:
A/Gene: CESP:DC2.3
A/Map position: 5
A/Intons: 65/2; 130/1; 150/3; 184/2; 217/2; 264/3; 303/3

Query Match 77.3%; Score 34; DB 2; Length 310;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPEE 8
Db 135 EPSAPPDE 142

RESULT 44

G84900
G-box binding bZIP transcription factor [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C/Accession: G84900
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Mottat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
eues, D.; Nleamat, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: G84900
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-382 <STO>
A/Cross-references: GB:AE002093; NID:g3702322; PIDN:AA62879.1; GSPDB:GN00139
C/Genetics:
A/Gene: At2g46270
A/Map position: 2
C/Superfamily: fava bean G-box-binding protein; fos/jun DNA-binding domain homology

Query Match 77.3%; Score 34; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPP 6
Db 16 KPSSPP 21

RESULT 45

UC7868
triacylglycerol lipase (EC 3.1.1.3) - Kurtzmanomyces sp. I-11
N/Alternate names: lipase; triacylglycerol acylhydrolase; tributyrase; triglyceride lipase
C/Species: Kurtzmanomyces sp. I-11
C/Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 31-Mar-2003
C/Accession: UC7868; PC7198
R/Kakugawa, K.; Shobayashi, M.; Suzuki, O.; Miyakawa, T.
Bioosci. Biotechnol. Biochem. 66, 1328-1336, 2002
A/Title: Cloning, characterization, and expression of cDNA encoding a lipase from Kurtzme
A/Reference number: UC7868; MUID:22152189; PMID:12162555

A/Accession: UC7868
A/Molecule type: mRNA
A/Residues: 1-458 <XAK>
A/Cross-references: DDBJ:AB073866
A/Accession: PC7198

A/Molecule type: protein
A/Residues: 27-56/133-152,188-207/301-317/340-357 <KA2>
C/Comment: This enzyme, which is a thermostable, acidophilic and position-non-specific ly
n of glycerides. Thus, this enzyme is useful as a catalyst in industry such as ester synt
C/Genetics:
A/Gene: lip1
C/Keywords: carboxylic ester hydrolase

Query Match 77.3%; Score 34; DB 2; Length 458;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPP 6
Db 96 KPSSPP 101

RESULT 46

A42401
macrophage elastase (EC 3.4.24.-) precursor - mouse
N/Alternate names: matrix metalloproteinase 12 (MMP12)
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C/Accession: A42401
R/Shapiro, S.D.; Griffin, G.L.; Gilbert, D.J.; Jenkins, N.A.; Copeland, N.G.; Welgus, H.C.
J. Biol. Chem. 267, 4664-4671, 1992
A/Title: Molecular cloning, chromosomal localization, and bacterial expression of a murin
A/Reference number: A42401; MUID:92165826; PMID:1537850
A/Accession: A42401
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-462 <SHA>

A/Cross-references: GB:M82831; NID:g199127; PIDN:AA35526.1; PID:g199128
C/Superfamily: Interstitial collagenase; hemopexin repeat homology; matrix metalloprotein
C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:53-256/Domain: matrix metalloproteinase homology <MMP>
F:269-462/Domain: hemopexin repeat homology <PXX>
F:85,211,215,221/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status i
F:211,215,221/Binding site: zinc, catalytic (His) (active) #status predicted
F:212/Active site: Glu #status predicted

Query Match 77.3%; Score 34; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPP 6
Db 266 KPSSPP 271

RESULT 47

FOVWLV

gag polyprotein - human immunodeficiency virus type 1 (isolate LAV-1a)

N:Alternate names: assemblin; core polyprotein; gag precursor

N:Contains: capsid antigen core protein p24CA; core protein p1; core protein p6; matrix

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 17-May-1985 #sequence_rev1501 17-May-1985 #text_change 05-Dec-1998

C:Accession: A03946

R:Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.

Cell 40, 9-11, 1985

A:Title: Nucleotide sequence of the AIDS virus, LAV.

A:Reference number: A90866; MUID:8509333; PMID:2981635

A:Accession: A03946

A:Molecule type: DNA

C:Genetics: 1-500 <WAI>

C:Superfamily: AIDS-related virus gag polyprotein

C:Keywords: AIDS; blocked amino end; core protein; immunodeficiency; lipoprotein; myrist

F:2-500/Product: gag precursor (assemblin) #status predicted <GAG>

F:2-132/Product: matrix antigen core protein p17MA #status predicted <P17>

F:20-32/Region: nuclear location signal

F:110-114/Region: nuclear location signal

F:133-363/Product: capsid antigen core protein p24CA #status predicted <P24>

F:164-377/Product: core protein p2 #status predicted <CP2>

F:178-432/Product: nucleocapsid core protein p1NC #status predicted <CP7>

F:192-405/Region: zinc finger CCHC motif

F:413-426/Region: zinc finger CCHC motif

F:433-448/Product: core protein p1 #status predicted <CP1>

F:449-500/Product: core protein p6 #status predicted <CP6>

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:132-395-400-405/Binding site: zinc (Cys, Cys, His, Cys) #status experimental

F:413-416-421-426/Binding site: zinc (Cys, Cys, His, Cys) #status experimental

Query Match

Best Local Similarity 77.3%; Score 34; DB 1; Length 500;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8

DB 454 EPTAPPEE 461

RESULT 48

FOVWLV

gag polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)

N:Alternate names: core polyprotein

N:Contains: core protein p15; core protein p17; core protein p24

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 30-Jun-1988 #sequence_rev1501 30-Jun-1988 #text_change 16-Jul-1999

C:Accession: A25523

R:Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, P.R.; Devare, Proc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986

A:Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human

A:Reference number: A94136; MUID:87041461; PMID:3490666

A:Accession: A25523

A:Molecule type: DNA

A:Residues: 1-500 <DES>

A:Cross-references: GB:M13136; NID:G326459; PIDN:AAA44306.1; PID:G326462

C:Genetics:

A:Gene: gag

C:Superfamily: AIDS-related virus gag polyprotein

C:Keywords: core protein; polyprotein

F:1-132/Product: core protein p17 #status predicted <P17>

F:133-391/Product: core protein p24 #status predicted <P24>

F:392-500/Product: core protein p15 #status predicted <P15>

Query Match

Best Local Similarity 77.3%; Score 34; DB 1; Length 500;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8

DB 454 EPTAPPEE 461

DB 454 EPTAPPEE 461

RESULT 49

gag polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence_rev1501 19-Mar-1997 #text_change 26-Aug-1999

C:Accession: S33979

R:Carlini, F.

submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33979

A:Molecule type: mRNA

A:Residues: 1-500 <CAR>

C:Cross-references: EMBL:Z1530; NID:G60192; PIDN:CAA77621.1; PID:G60193

C:Superfamily: AIDS-related virus gag polyprotein

Query Match

Best Local Similarity 77.3%; Score 34; DB 2; Length 500;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8

DB 454 EPTAPPEE 461

RESULT 50

FOVWLV

gag polyprotein - human immunodeficiency virus type 1 (isolate ARV-2)

N:Alternate names: core polyprotein

N:Contains: core protein p15; core protein p17; core protein p24

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C>Date: 17-May-1985 #sequence_rev1501 17-May-1985 #text_change 16-Jul-1999

C:Accession: A03947

R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stemple, M.M.; Brown-Shi

Science 227, 484-492, 1985

A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).

A:Reference number: A04003; MUID:85090453; PMID:2578227

A:Accession: A03947

A:Molecule type: DNA

A:Residues: 1-502 <SAN>

A:Cross-references: GB:K02007; NID:G328658; PIDN:AA59875.1; PID:G328661

C:Comment: Cleavage sites that yield the mature core proteins remain to be determined.

C:Genetics:

A:Gene: gag

C:Superfamily: AIDS-related virus gag polyprotein

C:Keywords: AIDS; core protein; immunodeficiency; polyprotein

F:1-134/Product: core protein p17 #status predicted <P17>

F:135-393/Product: core protein p24 #status predicted <P24>

F:394-502/Product: core protein p15 #status predicted <P15>

Query Match

Best Local Similarity 77.3%; Score 34; DB 1; Length 502;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSPPEE 8

DB 456 EPTAPPEE 463

Search completed: June 18, 2004, 13:00:26

Job time: 29 secs

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